

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	12357	(hepatitis adj c) or hcv-1	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L2	5504	hypervariable adj region	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L3	468	L1 and L2	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L4	56500	E2	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L5	253	L3 and L4	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L6	68191	consensus or motif	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L7	204	L5 and L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L8	204	L7	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:39
L9	306	MEFA	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:39
L10	13	I8 and I9	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:39



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- Search numbers may not be continuous; all searches are represented.
- Click on query # to add to strategy

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**Most Recent Queries**

**Time Result**

[#8](#) **Related Articles for PubMed (Select 10203493)**

16:36:58 [185](#)

[#7](#) **Search HCV assay multiple epitope fusion antigen E2**

16:36:56 [3](#)

[#6](#) **Search HCV assay multiple epitope fusion antigen**

16:36:05 [5](#)

[#5](#) **Search HCV assay NS3/4a multiple epitope fusion antigen**

16:35:53 [0](#)

[#4](#) **Search HCV assay NS3/4a MEFA**

16:35:42 [0](#)

[#3](#) **Search HCV assay NS3/4a**

16:35:29 [24](#)

[#2](#) **Search hepatitis C or HCV assay**

16:35:07 [35765](#)

[#1](#) **Search hepatitis C or HCV**

16:35:03 [36742](#)

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Jul 17 2006 06:31:01



# results of BLAST

BLASTP 2.2.14 [May-07-2006]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

**Reference:**

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153601903-10757-200512290520.BLASTQ4

**Database:** NCBI Protein Reference Sequences

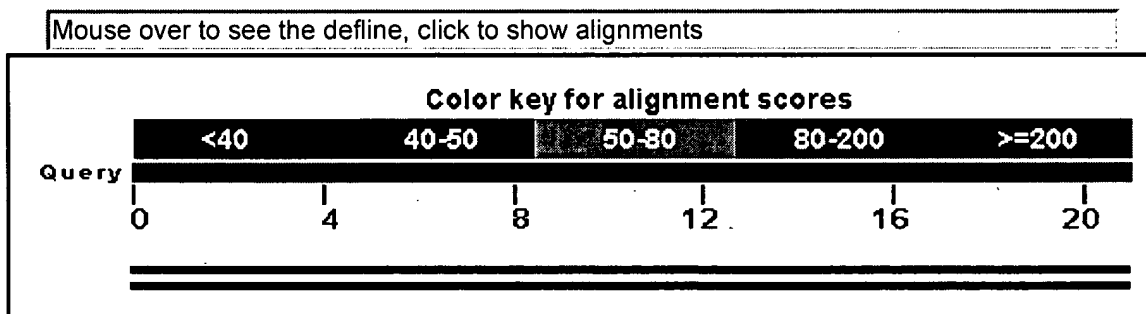
2,389,055 sequences; 864,113,167 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)  
[Taxonomy reports](#)

**Query=**

Length=21

## Distribution of 2 Blast Hits on the Query Sequence



[Distance tree of results](#) NEW

Sequences producing significant alignments:		Score (Bits)	E Value	
<a href="#">gi 26053623 ref NP_751921.1 </a>	E2 protein; viral envelope protein	<a href="#">34.7</a>	0.60	
<a href="#">gi 22129793 ref NP_671491.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	1.0	



Alignments

Get selected sequences

Select all

Deselect all

Distance tree of results

>  gi|26053623|ref|NP\_751921.1|  E2 protein; viral envelope protein [Hepatitis C virus]  
Length=363

Score = 34.7 bits (78), Expect = 0.60, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RTT+G V L PGAKQN  
Sbjct 7 GSAGRTTAGLVGLLTPGAKQN 27

>  gi|22129793|ref|NP\_671491.1|  polyprotein [Hepatitis C virus]  
Length=3011

Score = 34.3 bits (77), Expect = 1.0, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RTT+G V L PGAKQN  
Sbjct 390 GSAGRTTAGLVGLLTPGAKQN 410

Get selected sequences

Select all

Deselect all

Distance tree of results

Database: NCBI Protein Reference Sequences

Posted date: Jul 21, 2006 3:13 AM

Number of letters in database: 864,113,167

Number of sequences in database: 2,389,055

Lambda K H  
0.311 0.123 0.341

Gapped

Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 2389055

Number of Hits to DB: 6542300

Number of extensions: 52324

Number of successful extensions: 36

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 36

Number of HSP's successfully gapped: 0

Length of query: 21

Length of database: 864113167

Length adjustment: 0

Effective length of query: 21

Effective length of database: 864113167

Effective search space: 18146376507

Effective search space used: 18146376507

T: 11

A: 40

X1: 16 (7.2 bits)

X2: 38 (14.6 bits)



# results of BLAST

BLASTP 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153601814-24595-124256429206.BLASTQ4

Database: pat

301,733 sequences; 55,455,050 total letters

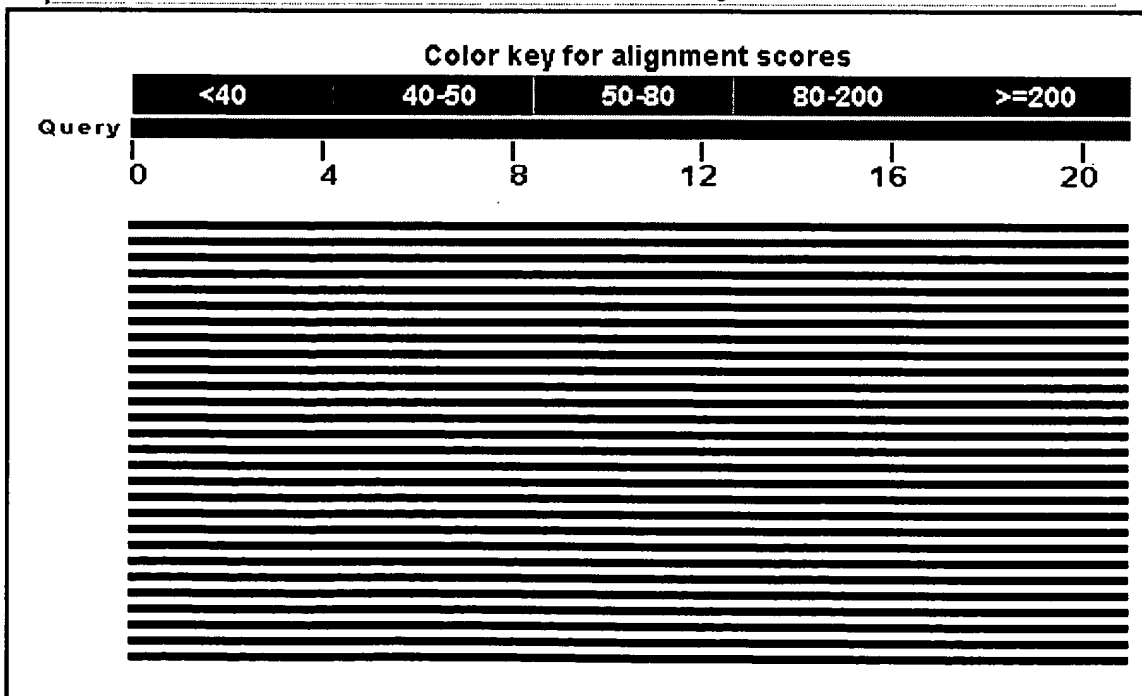
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)  
[Taxonomy reports](#)

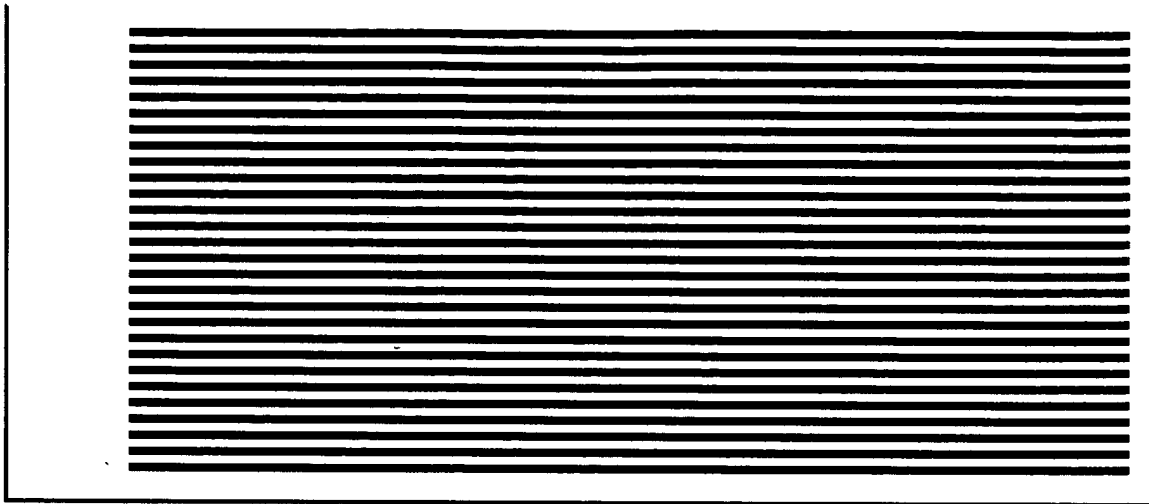
Query=

Length=21

## Distribution of 103 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments



Distance tree of results NEW

Sequences producing significant alignments:			Score (Bits)	E Value
<a href="#">gi 56627909 gb AAW06245.1 </a>	Sequence 4 from patent US 6797809 ...		<u>43.1</u>	1e-04
<a href="#">gi 40153769 gb AAR65055.1 </a>	Sequence 5 from patent US 6630298 ...		<u>42.0</u>	2e-04
<a href="#">gi 20221594 gb AAE87167.1 </a>	Sequence 3 from patent US 6326171 ...		<u>38.1</u>	0.003
<a href="#">gi 33759571 gb AAQ52061.1 </a>	Sequence 35 from patent US 6593083...		<u>38.1</u>	0.004
<a href="#">gi 33759570 gb AAQ52060.1 </a>	Sequence 34 from patent US 6593083...		<u>37.7</u>	0.005
<a href="#">gi 17912916 gb AAE83170.1 </a>	Sequence 14 from patent US 6303292...		<u>37.7</u>	0.005
<a href="#">gi 3993851 gb AAC87279.1 </a>	AR007645 Sequence 13 from patent US ...		<u>37.7</u>	0.005
<a href="#">gi 15108282 gb AAE67318.1 </a>	Sequence 39 from patent US 6210962...		<u>37.4</u>	0.006
<a href="#">gi 56567645 gb AAV98707.1 </a>	Sequence 7 from patent US 6740323 ...		<u>37.0</u>	0.008
<a href="#">gi 14101409 gb AAE53726.1 </a>	Sequence 89 from patent US 6150087		<u>37.0</u>	0.009
<a href="#">gi 31689077 gb AAP61048.1 </a>	Sequence 2 from patent US 6538123 ...		<u>36.6</u>	0.011
<a href="#">gi 593530 gb AAA55137.1 </a>	Sequence 2 from Patent EP 0388232		<u>36.6</u>	0.011
<a href="#">gi 21508650 gb AAM58139.1 </a>	Sequence 1 from patent US 6379886		<u>36.6</u>	0.011
<a href="#">gi 16239032 gb AAE78869.1 </a>	Sequence 3 from patent US 6274148 ...		<u>36.6</u>	0.011
<a href="#">gi 14101433 gb AAE53750.1 </a>	Sequence 138 from patent US 6150087		<u>36.6</u>	0.011
<a href="#">gi 14101424 gb AAE53741.1 </a>	Sequence 124 from patent US 6150087		<u>36.6</u>	0.011
<a href="#">gi 14124296 gb AAE60492.1 </a>	Sequence 6 from patent US 6194140 ...		<u>36.6</u>	0.011
<a href="#">gi 33759567 gb AAQ52057.1 </a>	Sequence 31 from patent US 6593083...		<u>36.2</u>	0.014
<a href="#">gi 14101452 gb AAE53769.1 </a>	Sequence 175 from patent US 6150087		<u>35.4</u>	0.023
<a href="#">gi 33737406 gb AAQ41059.1 </a>	Sequence 23 from patent US 6576417...		<u>35.4</u>	0.026
<a href="#">gi 14101440 gb AAE53757.1 </a>	Sequence 157 from patent US 6150087		<u>35.4</u>	0.026
<a href="#">gi 3993852 gb AAC87280.1 </a>	AR007646 Sequence 15 from patent US ...		<u>35.0</u>	0.033
<a href="#">gi 17912926 gb AAE83180.1 </a>	Sequence 24 from patent US 6303292...		<u>35.0</u>	0.036
<a href="#">gi 14101405 gb AAE53722.1 </a>	Sequence 81 from patent US 6150087		<u>34.7</u>	0.039
<a href="#">gi 40114092 gb AAR55231.1 </a>	Sequence 180 from patent US 661333...		<u>34.7</u>	0.041
<a href="#">gi 91149569 gb ABE23184.1 </a>	Sequence 2 from patent US 7009044		<u>34.7</u>	0.047
<a href="#">gi 33759566 gb AAQ52056.1 </a>	Sequence 30 from patent US 6593083...		<u>34.3</u>	0.058
<a href="#">gi 14101441 gb AAE53758.1 </a>	Sequence 158 from patent US 6150087		<u>34.3</u>	0.064
<a href="#">gi 91165235 gb ABE25678.1 </a>	Sequence 3 from patent US 7022323		<u>34.3</u>	0.064
<a href="#">gi 12828946 gb AAE50646.1 </a>	Sequence 2 from patent US 6127116		<u>34.3</u>	0.064
<a href="#">gi 14101448 gb AAE53765.1 </a>	Sequence 171 from patent US 6150087		<u>33.9</u>	0.074
<a href="#">gi 15108283 gb AAE67319.1 </a>	Sequence 40 from patent US 6210962...		<u>33.9</u>	0.075
<a href="#">gi 40114093 gb AAR55232.1 </a>	Sequence 181 from patent US 661333...		<u>33.9</u>	0.081
<a href="#">gi 77153553 emb CAJ33637.1 </a>	unnamed protein product [synthetic c		<u>33.9</u>	0.082
<a href="#">gi 77153498 emb CAJ33635.1 </a>	unnamed protein product [synthetic c		<u>33.5</u>	0.088
<a href="#">gi 3993854 gb AAC87282.1 </a>	AR007648 Sequence 19 from patent US ...		<u>33.5</u>	0.091
<a href="#">gi 17912919 gb AAE83173.1 </a>	Sequence 17 from patent US 6303292...		<u>33.5</u>	0.092
<a href="#">gi 17912922 gb AAE83176.1 </a>	Sequence 20 from patent US 6303292...		<u>33.5</u>	0.095

<a href="#">gi 15108276 gb AAE67312.1 </a>	Sequence 5 from patent US 6210962 ...	<a href="#">33.5</a>	0.099
<a href="#">gi 17912933 gb AAE83187.1 </a>	Sequence 31 from patent US 6303292...	<a href="#">33.5</a>	0.10
<a href="#">gi 77153551 emb CAJ33636.1 </a>	unnamed protein product [unidentifie	<a href="#">33.1</a>	0.11
<a href="#">gi 6001419 gb AAE22381.1 </a>	Sequence 4 from patent US 5854001 >...	<a href="#">33.1</a>	0.11
<a href="#">gi 42685373 gb AAS29954.1 </a>	Sequence 4 from patent US 6680059 ...	<a href="#">33.1</a>	0.13
<a href="#">gi 77153496 emb CAJ33634.1 </a>	unnamed protein product [Hepatitis C	<a href="#">33.1</a>	0.14
<a href="#">gi 75915319 gb ABA29873.1 </a>	Sequence 20 from patent US 6921634...	<a href="#">32.7</a>	0.16
<a href="#">gi 42685370 gb AAS29951.1 </a>	Sequence 1 from patent US 6680059 ...	<a href="#">32.7</a>	0.18
<a href="#">gi 2492381 gb AAB80517.1 I58189</a>	Sequence 13 from patent US 56100	<a href="#">32.7</a>	0.19
<a href="#">gi 2492387 gb AAB80523.1 I58195</a>	Sequence 19 from patent US 56100	<a href="#">32.3</a>	0.21
<a href="#">gi 2492389 gb AAB80525.1 I58197</a>	Sequence 21 from patent US 56100	<a href="#">32.3</a>	0.22
<a href="#">gi 51997479 emb CAH33883.1 </a>	unnamed protein product [syntheti...	<a href="#">32.3</a>	0.23
<a href="#">gi 2492384 gb AAB80520.1 I58192</a>	Sequence 16 from patent US 56100	<a href="#">32.3</a>	0.24
<a href="#">gi 2492383 gb AAB80519.1 I58191</a>	Sequence 15 from patent US 56100	<a href="#">32.3</a>	0.24
<a href="#">gi 17912934 gb AAE83188.1 </a>	Sequence 32 from patent US 6303292...	<a href="#">32.0</a>	0.25
<a href="#">gi 51997481 emb CAH33884.1 </a>	unnamed protein product [syntheti...	<a href="#">32.0</a>	0.25
<a href="#">gi 6001417 gb AAE22379.1 </a>	Sequence 1 from patent US 5854001 >...	<a href="#">32.0</a>	0.26
<a href="#">gi 12828947 gb AAE50647.1 </a>	Sequence 20 from patent US 6127116	<a href="#">32.0</a>	0.28
<a href="#">gi 6001418 gb AAE22380.1 </a>	Sequence 2 from patent US 5854001 >...	<a href="#">32.0</a>	0.28
<a href="#">gi 6001422 gb AAE22384.1 </a>	Sequence 10 from patent US 5854001 ...	<a href="#">32.0</a>	0.28
<a href="#">gi 2492388 gb AAB80524.1 I58196</a>	Sequence 20 from patent US 56100	<a href="#">32.0</a>	0.28
<a href="#">gi 2492386 gb AAB80522.1 I58194</a>	Sequence 18 from patent US 56100	<a href="#">32.0</a>	0.28
<a href="#">gi 17912925 gb AAE83179.1 </a>	Sequence 23 from patent US 6303292...	<a href="#">32.0</a>	0.29
<a href="#">gi 6001420 gb AAE22382.1 </a>	Sequence 6 from patent US 5854001 >...	<a href="#">32.0</a>	0.29
<a href="#">gi 3992567 gb AAC85994.1 AR005511</a>	Sequence 89 from patent US 574	<a href="#">32.0</a>	0.29
<a href="#">gi 2492380 gb AAB80516.1 I58188</a>	Sequence 12 from patent US 56100	<a href="#">32.0</a>	0.32
<a href="#">gi 2492376 gb AAB80512.1 I58184</a>	Sequence 7 from patent US 561000	<a href="#">31.6</a>	0.32
<a href="#">gi 3993850 gb AAC87278.1 AR007644</a>	Sequence 11 from patent US ...	<a href="#">31.6</a>	0.37
<a href="#">gi 3992566 gb AAC85993.1 AR005510</a>	Sequence 88 from patent US 574	<a href="#">31.6</a>	0.37
<a href="#">gi 40114091 gb AAR55230.1 </a>	Sequence 179 from patent US 661333...	<a href="#">31.2</a>	0.45
<a href="#">gi 3992568 gb AAC85995.1 AR005512</a>	Sequence 90 from patent US 574	<a href="#">31.2</a>	0.47
<a href="#">gi 6001423 gb AAE22385.1 </a>	Sequence 12 from patent US 5854001 ...	<a href="#">30.8</a>	0.60
<a href="#">gi 33759563 gb AAQ52053.1 </a>	Sequence 24 from patent US 6593083...	<a href="#">30.8</a>	0.64
<a href="#">gi 14101437 gb AAE53754.1 </a>	Sequence 150 from patent US 6150087	<a href="#">30.4</a>	0.75
<a href="#">gi 14101439 gb AAE53756.1 </a>	Sequence 156 from patent US 6150087	<a href="#">30.4</a>	0.85
<a href="#">gi 14101449 gb AAE53766.1 </a>	Sequence 172 from patent US 6150087	<a href="#">30.0</a>	1.1
<a href="#">gi 75915326 gb ABA29880.1 </a>	Sequence 40 from patent US 6921634	<a href="#">29.3</a>	1.8
<a href="#">gi 33767210 gb AAQ52972.1 </a>	Sequence 16 from patent US 6596476	<a href="#">28.9</a>	2.2
<a href="#">gi 91126690 gb ABE13381.1 </a>	Sequence 80 from patent US 6977144	<a href="#">28.9</a>	2.3
<a href="#">gi 3992487 gb AAC85914.1 AR005431</a>	Sequence 9 from patent US 5747	<a href="#">28.9</a>	2.5
<a href="#">gi 42713600 gb AAS36747.1 </a>	Sequence 50 from patent US 6692907...	<a href="#">28.9</a>	2.5
<a href="#">gi 40114102 gb AAR55240.1 </a>	Sequence 189 from patent US 661333...	<a href="#">28.9</a>	2.6
<a href="#">gi 42713619 gb AAS36766.1 </a>	Sequence 69 from patent US 6692907	<a href="#">28.1</a>	4.4
<a href="#">gi 911719 gb AAA71173.1 </a>	Sequence 8 from patent US 5428145	<a href="#">28.1</a>	4.4
<a href="#">gi 16219211 gb AAE73970.1 </a>	Sequence 36 from patent US 6245503...	<a href="#">28.1</a>	4.4
<a href="#">gi 16219221 gb AAE73976.1 </a>	Sequence 48 from patent US 6245503...	<a href="#">27.7</a>	4.8
<a href="#">gi 14101438 gb AAE53755.1 </a>	Sequence 152 from patent US 6150087	<a href="#">27.7</a>	5.0
<a href="#">gi 40160957 gb AAR67309.1 </a>	Sequence 30 from patent US 6635257...	<a href="#">27.7</a>	5.3
<a href="#">gi 16219219 gb AAE73975.1 </a>	Sequence 46 from patent US 6245503...	<a href="#">27.7</a>	5.4
<a href="#">gi 42713683 gb AAS36830.1 </a>	Sequence 133 from patent US 6692907	<a href="#">27.7</a>	5.5
<a href="#">gi 42713552 gb AAS36699.1 </a>	Sequence 2 from patent US 6692907	<a href="#">27.7</a>	5.5
<a href="#">gi 16219215 gb AAE73973.1 </a>	Sequence 42 from patent US 6245503...	<a href="#">27.7</a>	5.7
<a href="#">gi 42669271 gb AAS24964.1 </a>	Sequence 4 from patent US 6670114	<a href="#">27.7</a>	6.0
<a href="#">gi 16219223 gb AAE73977.1 </a>	Sequence 50 from patent US 6245503...	<a href="#">27.3</a>	6.3
<a href="#">gi 16219212 gb AAE73971.1 </a>	Sequence 38 from patent US 6245503...	<a href="#">27.3</a>	7.2
<a href="#">gi 40114103 gb AAR55241.1 </a>	Sequence 190 from patent US 661333...	<a href="#">27.3</a>	7.4
<a href="#">gi 4529993 emb CAA03144.1 </a>	unnamed protein product [unidentified	<a href="#">27.3</a>	7.6
<a href="#">gi 29370898 emb CAD86508.1 </a>	unnamed protein product [synthetic c	<a href="#">27.3</a>	7.8
<a href="#">gi 2492379 gb AAB80515.1 I58187</a>	Sequence 11 from patent US 56100	<a href="#">27.3</a>	7.8
<a href="#">gi 16219217 gb AAE73974.1 </a>	Sequence 44 from patent US 6245503...	<a href="#">27.3</a>	7.9
<a href="#">gi 12824387 gb AAE49293.1 </a>	Sequence 93 from patent US 6110465	<a href="#">27.3</a>	7.9

<u>gi 2492378 gb AAB80514.1 I58186</u>	Sequence 10 from patent US 56100	<u>27.3</u>	7.9
<u>gi 16219213 gb AAE73972.1 </u>	Sequence 40 from patent US 6245503...	<u>26.9</u>	7.9
<u>gi 40114118 gb AAR55252.1 </u>	Sequence 201 from patent US 661333...	<u>26.9</u>	8.3
<u>gi 3992565 gb AAC85992.1 AR005509</u>	Sequence 87 from patent US 574	<u>26.9</u>	8.5
<u>gi 2492385 gb AAB80521.1 I58193</u>	Sequence 17 from patent US 56100	<u>26.9</u>	9.5
<u>gi 14103322 gb AAE54756.1 </u>	Sequence 5 from patent US 6153421	<u>26.9</u>	9.8

## Alignments

Get selected sequences	Select all	Deselect all	Distance tree of results
------------------------	------------	--------------	--------------------------

> gi|56627909|gb|AAW06245.1| Sequence 4 from patent US 6797809  
gi|40158517|gb|AAR66374.1| Sequence 4 from patent US 6632601  
gi|21714050|emb|CAD38233.1| unnamed protein product [synthetic construct]  
Length=1099

Score = 43.1 bits (100), Expect = 1e-04, Method: Composition-based stats.  
Identities = 21/21 (100%), Positives = 21/21 (100%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSGFVSLFAPGAKQN  
Sbjct 179 GSAARTTSGFVSLFAPGAKQN 199

Score = 35.4 bits (80), Expect = 0.022, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+AARTTSG SLF+PGA QN  
Sbjct 206 GAAARTTSGLTSLFSPGASQN 226

> gi|40153769|gb|AAR65055.1| Sequence 5 from patent US 6630298  
gi|21066311|emb|CAD32155.1| unnamed protein product [synthetic construct]  
Length=829

Score = 42.0 bits (97), Expect = 2e-04, Method: Composition-based stats.  
Identities = 21/21 (100%), Positives = 21/21 (100%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSGFVSLFAPGAKQN  
Sbjct 92 GSAARTTSGFVSLFAPGAKQN 112

Score = 34.7 bits (78), Expect = 0.039, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+AARTTSG SLF+PGA QN  
Sbjct 119 GAAARTTSGLTSLFSPGASQN 139

> gi|20221594|gb|AAE87167.1| Sequence 3 from patent US 6326171  
gi|29718028|gb|AAP01124.1| Sequence 4 from patent US 6521423  
Length=663

Score = 38.1 bits (87), Expect = 0.003, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)



# results of BLAST

BLASTP 2.2.14 [May-07-2006]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

**Reference:**

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

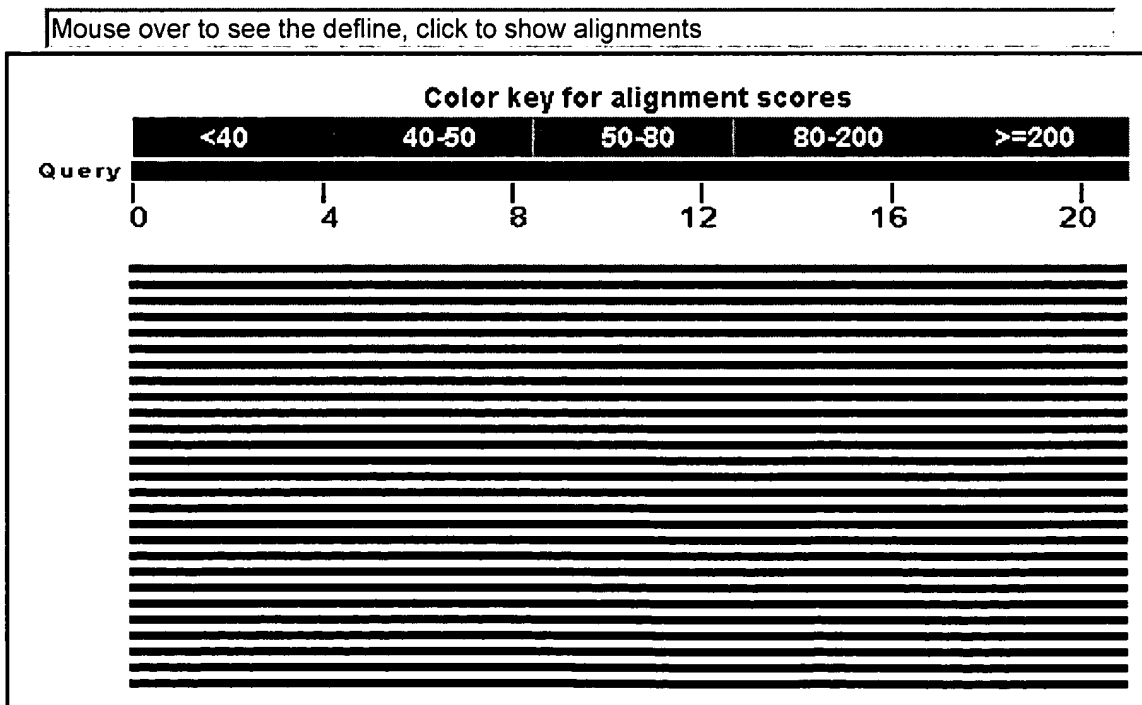
RID: 1153601291-14310-20277516180.BLASTQ1

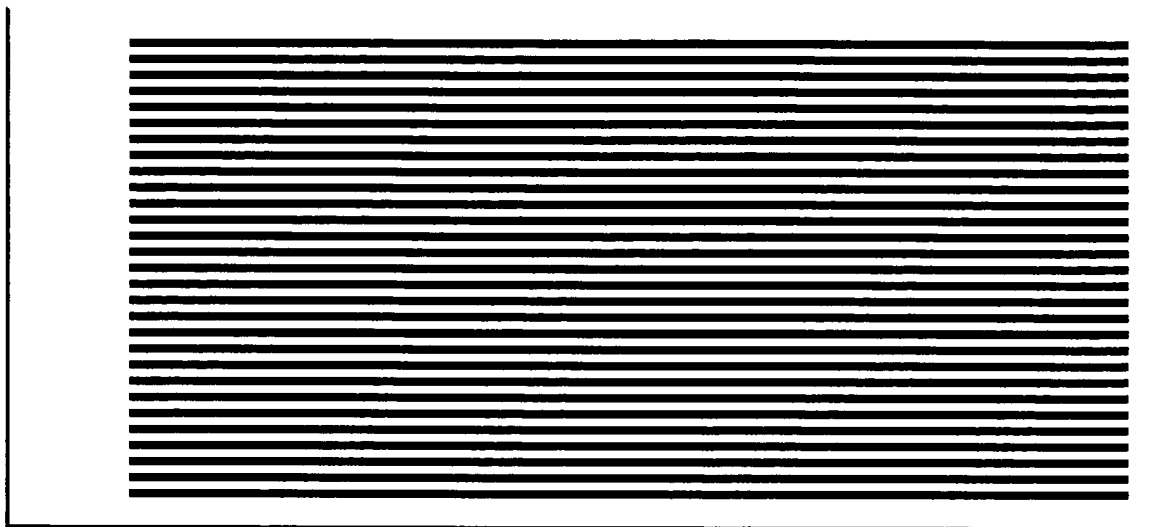
**Database:** All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF excluding environmental samples  
3,807,609 sequences; 1,312,719,415 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)  
[Taxonomy reports](#)

**Query=**  
Length=21

## Distribution of 100 Blast Hits on the Query Sequence



Distance tree of results 

Sequences producing significant alignments:			Score (Bits)	E Value
<a href="#">gi 58198305 gb AAW65860.1 </a>	envelope protein [synthetic construct		41.2	0.010
<a href="#">gi 64501453 gb AAAY41694.1 </a>	envelope [Hepatitis C virus]		41.2	0.011
<a href="#">gi 58198313 gb AAW65864.1 </a>	envelope protein [synthetic construct		41.2	0.011
<a href="#">gi 58198309 gb AAW65862.1 </a>	envelope protein [synthetic construct		41.2	0.011
<a href="#">gi 64501451 gb AAAY41693.1 </a>	envelope [Hepatitis C virus]		41.2	0.011
<a href="#">gi 64501435 gb AAAY41685.1 </a>	envelope [Hepatitis C virus]		41.2	0.012
<a href="#">gi 58198311 gb AAW65863.1 </a>	envelope protein [synthetic construct		41.2	0.012
<a href="#">gi 64501449 gb AAAY41692.1 </a>	envelope [Hepatitis C virus]		41.2	0.012
<a href="#">gi 64501447 gb AAAY41691.1 </a>	envelope [Hepatitis C virus]		41.2	0.012
<a href="#">gi 2565261 gb AAC61802.1 </a>	E2/NS1 protein [Hepatitis C virus]		39.7	0.030
<a href="#">gi 15341438 gb AAK95634.1 </a>	polyprotein [Hepatitis C virus]		39.7	0.031
<a href="#">gi 58220842 gb AAW68049.1 </a>	envelope protein [synthetic construct		39.3	0.037
<a href="#">gi 64501419 gb AAAY41677.1 </a>	envelope [Hepatitis C virus] >gi 6...		39.3	0.042
<a href="#">gi 64501423 gb AAAY41679.1 </a>	envelope [Hepatitis C virus]		39.3	0.044
<a href="#">gi 64501439 gb AAAY41687.1 </a>	envelope [Hepatitis C virus]		39.3	0.044
<a href="#">gi 64501427 gb AAAY41681.1 </a>	envelope [Hepatitis C virus]		39.3	0.044
<a href="#">gi 64501445 gb AAAY41690.1 </a>	envelope [Hepatitis C virus]		39.3	0.046
<a href="#">gi 13448566 gb AAK27104.1 </a>	polyprotein [Hepatitis C virus]		38.1	0.099
<a href="#">gi 58198307 gb AAW65861.1 </a>	envelope protein [synthetic construct		37.7	0.13
<a href="#">gi 64501455 gb AAAY41695.1 </a>	envelope [Hepatitis C virus]		37.7	0.13
<a href="#">gi 64501429 gb AAAY41682.1 </a>	envelope [Hepatitis C virus]		37.7	0.14
<a href="#">gi 33337015 gb AAQ13175.1 </a>	polyprotein [Hepatitis C virus]		37.0	0.20
<a href="#">gi 64501425 gb AAAY41680.1 </a>	truncated envelope [Hepatitis C vi...		37.0	0.20
<a href="#">gi 53801738 gb AAU94042.1 </a>	polyprotein [Hepatitis C virus] >g...		37.0	0.21
<a href="#">gi 16518692 gb AAL24947.1 </a>	glycoprotein [Hepatitis C virus]		37.0	0.23
<a href="#">gi 13448510 gb AAK27077.1 </a>	polyprotein [Hepatitis C virus].		37.0	0.23
<a href="#">gi 33337023 gb AAQ13179.1 </a>	polyprotein [Hepatitis C virus]		36.6	0.24
<a href="#">gi 53801728 gb AAU94037.1 </a>	polyprotein [Hepatitis C virus]		36.6	0.25
<a href="#">gi 13448516 gb AAK27080.1 </a>	polyprotein [Hepatitis C virus]		36.6	0.25
<a href="#">gi 130455 sp P26664 POLG HCV1</a>	Genome polyprotein [Contains: C...		36.6	0.26
<a href="#">gi 67810851 gb AAAY82013.1 </a>	polyprotein [Hepatitis C virus]		36.6	0.26
<a href="#">gi 67810849 gb AAAY82012.1 </a>	polyprotein [Hepatitis C virus]		36.6	0.26
<a href="#">gi 14532249 gb AAK66556.1 </a>	HCV type 1a/1b chimera polyprotein...		36.6	0.26
<a href="#">gi 14532251 gb AAK66557.1 </a>	HCV type 1a/1b chimera mutant polypro		36.6	0.26
<a href="#">gi 53801732 gb AAU94039.1 </a>	polyprotein [Hepatitis C virus]		36.6	0.27
<a href="#">gi 33337057 gb AAQ13196.1 </a>	polyprotein [Hepatitis C virus] >g...		36.6	0.28
<a href="#">gi 37957242 gb AAP03950.1 </a>	polyprotein [Hepatitis C virus]		36.6	0.28

<a href="#">gi 436988 qb AAA45601.1 </a>	putative	36.6	0.28
<a href="#">gi 7649227 qb AAF65803.1 </a>	polyprotein precursor [Hepatitis C vir	36.6	0.30
<a href="#">gi 37957231 qb AAP03945.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.32
<a href="#">gi 33337017 qb AAQ13176.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.32
<a href="#">gi 33337005 qb AAQ13170.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.32
<a href="#">gi 67810855 qb AAQ82015.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.32
<a href="#">gi 67810853 qb AAQ82014.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.32
<a href="#">gi 13448514 qb AAK27079.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.33
<a href="#">gi 7670859 qb AAF66249.1 </a>	polyprotein precursor [Hepatitis C vir	36.2	0.34
<a href="#">gi 33336981 qb AAQ13158.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.34
<a href="#">gi 4469531 qb AAD21305.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.34
<a href="#">gi 33337045 qb AAQ13190.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.36
<a href="#">gi 13448244 qb AAK26946.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.36
<a href="#">gi 33337025 qb AAQ13180.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.36
<a href="#">gi 33337021 qb AAQ13178.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.36
<a href="#">gi 33336921 qb AAQ13128.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.36
<a href="#">gi 53802198 qb AAU94270.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.38
<a href="#">gi 13448555 qb AAK27099.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.39
<a href="#">gi 33336927 qb AAQ13131.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.39
<a href="#">gi 37957251 qb AAP03954.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.40
<a href="#">gi 37957229 qb AAP03944.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.40
<a href="#">gi 33336925 qb AAQ13130.1 </a>	polyprotein [Hepatitis C virus] >g...	36.2	0.40
<a href="#">gi 33336495 qb AAQ12915.1 </a>	polyprotein [Hepatitis C virus]	36.2	0.40
<a href="#">gi 33337001 qb AAQ13168.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.40
<a href="#">gi 13344963 qb AAK19135.1 </a>	polyprotein precursor [Hepatitis C vi	35.8	0.41
<a href="#">gi 7670871 qb AAF66255.1 </a>	polyprotein precursor [Hepatitis C vir	35.8	0.41
<a href="#">gi 53802217 qb AAU94278.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.41
<a href="#">gi 33336881 qb AAQ13108.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.41
<a href="#">gi 37957244 qb AAP03951.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.41
<a href="#">gi 37957239 qb AAP03949.1 </a>	polyprotein [Hepatitis C virus] >g...	35.8	0.42
<a href="#">gi 33336889 qb AAQ13112.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.42
<a href="#">gi 13448238 qb AAK26943.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.42
<a href="#">gi 7670919 qb AAF66279.1 </a>	polyprotein precursor [Hepatitis C vir	35.8	0.42
<a href="#">gi 7670867 qb AAF66253.1 </a>	polyprotein precursor [Hepatitis C vir	35.8	0.42
<a href="#">gi 33336867 qb AAQ13101.1 </a>	polyprotein [Hepatitis C virus] >g...	35.8	0.43
<a href="#">gi 33336885 qb AAQ13110.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.44
<a href="#">gi 16518684 qb AAL24943.1 </a>	glycoprotein [Hepatitis C virus]	35.8	0.44
<a href="#">gi 7670861 qb AAF66250.1 </a>	polyprotein precursor [Hepatitis C vir	35.8	0.44
<a href="#">gi 7670939 qb AAF66289.1 </a>	polyprotein precursor [Hepatitis C vir	35.8	0.45
<a href="#">gi 33336909 qb AAQ13122.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.47
<a href="#">gi 4927491 qb AAD33137.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.47
<a href="#">gi 37957257 qb AAP03957.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.48
<a href="#">gi 13448474 qb AAK27059.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.49
<a href="#">gi 37957255 qb AAP03956.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.50
<a href="#">gi 13448502 qb AAK27073.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.50
<a href="#">gi 37957179 qb AAP03919.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.50
<a href="#">gi 13448524 qb AAK27084.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.51
<a href="#">gi 37957249 qb AAP03953.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.52
<a href="#">gi 37957246 qb AAP03952.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.52
<a href="#">gi 33336887 qb AAQ13111.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.52
<a href="#">gi 53801742 qb AAU94044.1 </a>	polyprotein [Hepatitis C virus]	35.8	0.52
<a href="#">gi 4927589 qb AAD33166.1 </a>	polyprotein [Hepatitis C virus]	35.4	0.55
<a href="#">gi 4927496 qb AAD33142.1 </a>	polyprotein [Hepatitis C virus] >gi...	35.4	0.55
<a href="#">gi 53801730 qb AAU94038.1 </a>	polyprotein [Hepatitis C virus]	35.4	0.55
<a href="#">gi 51558189 qb AAU06654.1 </a>	envelope glycoprotein [Hepatitis C vi	35.4	0.56
<a href="#">gi 53801726 qb AAU94036.1 </a>	polyprotein [Hepatitis C virus]	35.4	0.56
<a href="#">gi 53801734 qb AAU94040.1 </a>	polyprotein [Hepatitis C virus]	35.4	0.57
<a href="#">gi 33336863 qb AAQ13099.1 </a>	polyprotein [Hepatitis C virus]	35.4	0.57
<a href="#">gi 38539525 qb AAR23635.1 </a>	polyprotein [Hepatitis C virus]	35.4	0.58
<a href="#">gi 221688 dbj BAA14118.1 </a>	X protein [Hepatitis C virus]	35.4	0.58
<a href="#">gi 37957233 qb AAP03946.1 </a>	polyprotein [Hepatitis C virus]	35.4	0.59

gi 53801718 qb AAU94032.1	polyprotein [Hepatitis C virus]	35.4	0.59
gi 33336821 qb AAQ13078.1	polyprotein [Hepatitis C virus]	35.4	0.59
gi 4927621 qb AAD33198.1	polyprotein [Hepatitis C virus]	35.4	0.60
gi 4927579 qb AAD33156.1	polyprotein [Hepatitis C virus]	35.4	0.63
gi 33336839 qb AAQ13087.1	polyprotein [Hepatitis C virus]	35.4	0.64
gi 7670905 qb AAF66272.1	polyprotein precursor [Hepatitis C vir	35.4	0.64
gi 13448551 qb AAK27097.1	polyprotein [Hepatitis C virus]	35.4	0.66
gi 13344959 qb AAK19133.1	polyprotein precursor [Hepatitis C vi	35.4	0.66
gi 33336865 qb AAQ13100.1	polyprotein [Hepatitis C virus]	35.4	0.66
gi 16518694 qb AAL24948.1	glycoprotein [Hepatitis C virus] >...	35.4	0.67
gi 13448545 qb AAK27094.1	polyprotein [Hepatitis C virus] >g...	35.4	0.67
gi 13448541 qb AAK27092.1	polyprotein [Hepatitis C virus]	35.4	0.67
gi 33336851 qb AAQ13093.1	polyprotein [Hepatitis C virus]	35.0	0.70
gi 13448539 qb AAK27091.1	polyprotein [Hepatitis C virus]	35.0	0.71
gi 33336931 qb AAQ13133.1	polyprotein [Hepatitis C virus] >g...	35.0	0.71
gi 4927584 qb AAD33161.1	polyprotein [Hepatitis C virus]	35.0	0.71
gi 4927575 qb AAD33152.1	polyprotein [Hepatitis C virus]	35.0	0.71
gi 53801809 qb AAU94077.1	polyprotein [Hepatitis C virus]	35.0	0.72
gi 53801937 qb AAU94141.1	polyprotein [Hepatitis C virus]	35.0	0.73
gi 221587 dbj BAA01582.1	polyprotein precursor [Hepatitis C vir	35.0	0.76
gi 13448316 qb AAK26981.1	polyprotein [Hepatitis C virus] >g...	35.0	0.77
gi 33336823 qb AAQ13079.1	polyprotein [Hepatitis C virus]	35.0	0.77
gi 13448620 qb AAK27131.1	polyprotein [Hepatitis C virus]	35.0	0.77
gi 33336861 qb AAQ13098.1	polyprotein [Hepatitis C virus] >g...	35.0	0.79
gi 53801951 qb AAU94147.1	polyprotein [Hepatitis C virus]	35.0	0.79
gi 13448549 qb AAK27096.1	polyprotein [Hepatitis C virus]	35.0	0.80
gi 13448320 qb AAK26983.1	polyprotein [Hepatitis C virus]	35.0	0.80
gi 13448588 qb AAK27115.1	polyprotein [Hepatitis C virus] >g...	35.0	0.81
gi 53802206 qb AAU94273.1	polyprotein [Hepatitis C virus]	35.0	0.81
gi 89519415 qb ABD75829.1	polyprotein [Hepatitis C virus]	35.0	0.81
gi 33336965 qb AAQ13150.1	polyprotein [Hepatitis C virus]	35.0	0.82
gi 13448326 qb AAK26986.1	polyprotein [Hepatitis C virus]	35.0	0.82
gi 33337033 qb AAQ13184.1	polyprotein [Hepatitis C virus]	35.0	0.83
gi 13448314 qb AAK26980.1	polyprotein [Hepatitis C virus]	35.0	0.84
gi 56406500 qb AAV87599.1	polyprotein [Hepatitis C virus]	35.0	0.85
gi 33336761 qb AAQ13048.1	polyprotein [Hepatitis C virus]	35.0	0.85
gi 13448578 qb AAK27110.1	polyprotein [Hepatitis C virus]	35.0	0.86
gi 33637194 qb AAQ23753.1	polyprotein [Hepatitis C virus]	35.0	0.86
gi 33336525 qb AAQ12930.1	polyprotein [Hepatitis C virus]	35.0	0.87
gi 13448322 qb AAK26984.1	polyprotein [Hepatitis C virus]	35.0	0.87
gi 33336639 qb AAQ12987.1	polyprotein [Hepatitis C virus]	35.0	0.89
gi 13448318 qb AAK26982.1	polyprotein [Hepatitis C virus]	35.0	0.89
gi 53801935 qb AAU94140.1	polyprotein [Hepatitis C virus]	35.0	0.89
gi 33336815 qb AAQ13075.1	polyprotein [Hepatitis C virus]	35.0	0.89
gi 7649241 qb AAF65810.1	polyprotein precursor [Hepatitis C vir	34.7	0.90
gi 109259768 qb AAW65879.2	envelope protein [synthetic construc	34.7	0.90
gi 13448296 qb AAK26971.1	polyprotein [Hepatitis C virus]	34.7	0.91
gi 13448294 qb AAK26970.1	polyprotein [Hepatitis C virus]	34.7	0.91
gi 53801948 qb AAU94146.1	polyprotein [Hepatitis C virus]	34.7	0.91
gi 26053623 ref NP_751921.1	E2 protein; viral envelope protein	34.7	0.91
gi 13448580 qb AAK27111.1	polyprotein [Hepatitis C virus]	34.7	0.92
gi 64501433 qb AAY41684.1	envelope [Hepatitis C virus]	34.7	0.92
gi 37957282 qb AAP03969.1	polyprotein [Hepatitis C virus]	34.7	0.92
gi 58198303 qb AAW65859.1	envelope protein [synthetic construct	34.7	0.93
gi 33336957 qb AAQ13146.1	polyprotein [Hepatitis C virus]	34.7	0.95
gi 7649243 qb AAF65811.1	polyprotein precursor [Hepatitis C vir	34.7	0.96
gi 109259770 qb AAW65880.2	envelope protein [synthetic construc	34.7	0.98
gi 64501431 qb AAY41683.1	envelope [Hepatitis C virus]	34.7	0.98
gi 33336563 qb AAQ12949.1	polyprotein [Hepatitis C virus]	34.7	0.99
gi 7649239 qb AAF65809.1	polyprotein precursor [Hepatitis C vir	34.7	0.99
gi 7649247 qb AAF65813.1	polyprotein precursor [Hepatitis C vir	34.7	1.0



<a href="#">gi 94317855 gb ABF15187.1 </a>	polyprotein precursor [Hepatitis C vi	<a href="#">34.7</a>	<a href="#">1.0</a>
<a href="#">gi 7670903 gb AAF66271.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">34.7</a>	<a href="#">1.0</a>
<a href="#">gi 64501443 gb AAY41689.1 </a>	envelope [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.0</a>
<a href="#">gi 33336997 gb AAQ13166.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">34.7</a>	<a href="#">1.0</a>
<a href="#">gi 7649237 gb AAF65808.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">34.7</a>	<a href="#">1.0</a>
<a href="#">gi 33336507 gb AAQ12921.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.0</a>
<a href="#">gi 4469530 gb AAD21304.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 50235322 gb AAT69968.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 33637202 gb AAQ23757.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 7649233 gb AAF65806.1 </a>	polyprotein precursor [Hepatitis C ...	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 33637208 gb AAQ23760.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 7670911 gb AAF66275.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 7670863 gb AAF66251.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 53801865 gb AAU94105.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 13448285 gb AAK26966.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 7649235 gb AAF65807.1 </a>	polyprotein precursor [Hepatitis C ...	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 4927576 gb AAD33153.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 33336831 gb AAQ13083.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 33336779 gb AAQ13057.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 33336661 gb AAQ12998.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.1</a>
<a href="#">gi 13448354 gb AAK27000.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.2</a>
<a href="#">gi 84380361 gb ABC58410.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.7</a>	<a href="#">1.2</a>
<a href="#">gi 37957197 gb AAP03928.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 5918965 gb AAD56198.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 90658415 gb ABD97104.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 13448290 gb AAK26968.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 33336593 gb AAQ12964.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 33637190 gb AAQ23751.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 13448352 gb AAK26999.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 13448287 gb AAK26967.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 33336539 gb AAQ12937.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 33337031 gb AAQ13183.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 33336801 gb AAQ13068.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 7649251 gb AAF65815.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">34.3</a>	<a href="#">1.2</a>
<a href="#">gi 37957131 gb AAP03895.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 56342211 dbj BAD73983.1 </a>	polyprotein [Hepatitis C virus type	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 33336659 gb AAQ12997.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 7649249 gb AAF65814.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 33336725 gb AAQ13030.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 33336535 gb AAQ12935.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 13448283 gb AAK26965.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 33336973 gb AAQ13154.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 58220848 gb AAW68051.1 </a>	envelope protein [synthetic construct	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 33336543 gb AAQ12939.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 62554071 dbj BAD95611.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 33637198 gb AAQ23755.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.3</a>
<a href="#">gi 33336877 gb AAQ13106.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.4</a>
<a href="#">gi 33336983 gb AAQ13159.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.4</a>
<a href="#">gi 13448646 gb AAK27144.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.4</a>
<a href="#">gi 13344957 gb AAK19132.1 </a>	polyprotein precursor [Hepatitis C vi	<a href="#">34.3</a>	<a href="#">1.4</a>
<a href="#">gi 7670915 gb AAF66277.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">34.3</a>	<a href="#">1.4</a>
<a href="#">gi 33336663 gb AAQ12999.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.4</a>
<a href="#">gi 33336929 gb AAQ13132.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.4</a>
<a href="#">gi 33637206 gb AAQ23759.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.4</a>
<a href="#">gi 7670913 gb AAF66276.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">34.3</a>	<a href="#">1.4</a>
<a href="#">gi 7650256 gb AAF65959.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.4</a>
<a href="#">gi 84380358 gb ABC58409.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">34.3</a>	<a href="#">1.4</a>
<a href="#">gi 59474 emb CAA37292.1 </a>	unnamed protein product [Hepatitis C vi	<a href="#">34.3</a>	<a href="#">1.5</a>
<a href="#">gi 4927628 gb AAD33205.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.5</a>
<a href="#">gi 4927605 gb AAD33182.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.5</a>
<a href="#">gi 4927572 gb AAD33149.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">34.3</a>	<a href="#">1.5</a>

<a href="#">gi 33637212 gb AAQ23762.1 </a>	polyprotein [Hepatitis C virus]	34.3	1.5
<a href="#">gi 33336529 gb AAQ12932.1 </a>	polyprotein [Hepatitis C virus]	34.3	1.5
<a href="#">gi 16518682 gb AAL24942.1 </a>	glycoprotein [Hepatitis C virus] >...	34.3	1.5
<a href="#">gi 20340011 gb AAM19658.1 </a>	E1/E2 protein [Hepatitis C virus]	34.3	1.5
<a href="#">gi 4469527 gb AAD21301.1 </a>	polyprotein [Hepatitis C virus]	34.3	1.5
<a href="#">gi 33336945 gb AAQ13140.1 </a>	polyprotein [Hepatitis C virus]	34.3	1.5
<a href="#">gi 13448234 gb AAK26941.1 </a>	polyprotein [Hepatitis C virus]	34.3	1.5
<a href="#">gi 22129793 ref NP_671491.1 </a>	polyprotein [Hepatitis C virus] ...	34.3	1.5
<a href="#">gi 4927597 gb AAD33174.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.5
<a href="#">gi 33336781 gb AAQ13058.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.6
<a href="#">gi 33336511 gb AAQ12923.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.6
<a href="#">gi 33336481 gb AAQ12908.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.6
<a href="#">gi 7670929 gb AAF66284.1 </a>	polyprotein precursor [Hepatitis C vir	33.9	1.6
<a href="#">gi 13448266 gb AAK26957.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.6
<a href="#">gi 33336755 gb AAQ13045.1 </a>	polyprotein [Hepatitis C virus] >g...	33.9	1.6
<a href="#">gi 23955759 gb AAN40611.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.6
<a href="#">gi 13344961 gb AAK19134.1 </a>	polyprotein precursor [Hepatitis C vi	33.9	1.6
<a href="#">gi 4469528 gb AAD21302.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 13448232 gb AAK26940.1 </a>	polyprotein [Hepatitis C virus] >g...	33.9	1.7
<a href="#">gi 13448226 gb AAK26937.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 4927608 gb AAD33185.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 4927622 gb AAD33199.1 </a>	polyprotein [Hepatitis C virus] >gi...	33.9	1.7
<a href="#">gi 4927568 gb AAD33145.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 20340013 gb AAM19659.1 </a>	E1/E2 protein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 221512 dbj BAA00705.1 </a>	structural protein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 33336795 gb AAQ13065.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 33336763 gb AAQ13049.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 13448454 gb AAK27049.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 53801722 gb AAU94034.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 6521009 dbj BAA88057.1 </a>	polyprotein [Hepatitis C virus (is...	33.9	1.7
<a href="#">gi 33637210 gb AAQ23761.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 13448478 gb AAK27061.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 4927632 gb AAD33209.1 </a>	polyprotein [Hepatitis C virus] >gi...	33.9	1.7
<a href="#">gi 13448292 gb AAK26969.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 13448224 gb AAK26936.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.7
<a href="#">gi 20340017 gb AAM19661.1 </a>	E1/E2 protein [Hepatitis C virus] ...	33.9	1.7
<a href="#">gi 1372958 gb AAB02127.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 30025530 gb AAP04379.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 4927629 gb AAD33206.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 4927609 gb AAD33186.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 4927631 gb AAD33208.1 </a>	polyprotein [Hepatitis C virus] >gi...	33.9	1.8
<a href="#">gi 4927580 gb AAD33157.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 33336509 gb AAQ12922.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 22385223 gb AAM96142.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 13448330 gb AAK26988.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 13448260 gb AAK26954.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 4469529 gb AAD21303.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 33336731 gb AAQ13033.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 23955751 gb AAN40607.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 23955749 gb AAN40606.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 33336749 gb AAQ13042.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 33336717 gb AAQ13026.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 13448220 gb AAK26934.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 4927611 gb AAD33188.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 4927604 gb AAD33181.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 4927600 gb AAD33177.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 4927595 gb AAD33172.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 4927620 gb AAD33197.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.8
<a href="#">gi 33336645 gb AAQ12990.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.9
<a href="#">gi 33637200 gb AAQ23756.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.9
<a href="#">gi 29647945 gb AAO87872.1 </a>	polyprotein [Hepatitis C virus]	33.9	1.9

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<a href="#">gi 13448228 gb AAK26938.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	1.9
<a href="#">gi 13448222 gb AAK26935.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	1.9
<a href="#">gi 4927633 gb AAD33210.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	1.9
<a href="#">gi 4927615 gb AAD33192.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	1.9
<a href="#">gi 4927585 gb AAD33162.1 </a>	polyprotein [Hepatitis C virus] >gi...	<a href="#">33.9</a>	1.9
<a href="#">gi 436992 gb AAA45602.1 </a>	putative	<a href="#">33.9</a>	1.9
<a href="#">gi 37957253 gb AAP03955.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	1.9
<a href="#">gi 33637196 gb AAQ23754.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	1.9
<a href="#">gi 16518644 gb AAL24923.1 </a>	glycoprotein [Hepatitis C virus]	<a href="#">33.9</a>	1.9
<a href="#">gi 13448447 gb AAK27046.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	1.9
<a href="#">gi 13448332 gb AAK26989.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	1.9
<a href="#">gi 67810875 gb AA82024.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">33.9</a>	1.9
<a href="#">gi 4469504 gb AAD21278.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	1.9
<a href="#">gi 436990 gb AAA72391.1 </a>	[Hepatitis C virus gene, partial cds.],	<a href="#">33.9</a>	1.9
<a href="#">gi 13448328 gb AAK26987.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	1.9
<a href="#">gi 13448312 gb AAK26979.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	2.0
<a href="#">gi 4469514 gb AAD21288.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	2.0
<a href="#">gi 20340019 gb AAM19662.1 </a>	E1/E2 protein [Hepatitis C virus] ...	<a href="#">33.9</a>	2.0
<a href="#">gi 7670873 gb AAF66256.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">33.9</a>	2.0
<a href="#">gi 4927606 gb AAD33183.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	2.0
<a href="#">gi 4927603 gb AAD33180.1 </a>	polyprotein [Hepatitis C virus] >gi...	<a href="#">33.9</a>	2.0
<a href="#">gi 4469505 gb AAD21279.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	2.0
<a href="#">gi 13448476 gb AAK27060.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	2.0
<a href="#">gi 20339987 gb AAM19646.1 </a>	E1/E2 protein [Hepatitis C virus] ...	<a href="#">33.9</a>	2.0
<a href="#">gi 16517602 gb AAL24763.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.9</a>	2.0
<a href="#">gi 40389093 gb AAR85724.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.5</a>	2.0
<a href="#">gi 13344951 gb AAK19129.1 </a>	polyprotein precursor [Hepatitis C vi	<a href="#">33.5</a>	2.0
<a href="#">gi 16517673 gb AAL24798.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.0
<a href="#">gi 56342217 dbj BAD73986.1 </a>	polyprotein [Hepatitis C virus type	<a href="#">33.5</a>	2.0
<a href="#">gi 4927625 gb AAD33202.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.0
<a href="#">gi 4927627 gb AAD33204.1 </a>	polyprotein [Hepatitis C virus] >gi...	<a href="#">33.5</a>	2.0
<a href="#">gi 4927626 gb AAD33203.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.0
<a href="#">gi 37957173 gb AAP03916.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.0
<a href="#">gi 33336859 gb AAQ13097.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.0
<a href="#">gi 16517620 gb AAL24772.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.0
<a href="#">gi 20339983 gb AAM19644.1 </a>	E1/E2 protein [Hepatitis C virus] ...	<a href="#">33.5</a>	2.0
<a href="#">gi 46403731 gb AAS92927.1 </a>	E1E2 region of HCV polyprotein [sy...	<a href="#">33.5</a>	2.0
<a href="#">gi 7670865 gb AAF66252.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">33.5</a>	2.1
<a href="#">gi 40389227 gb AAR85791.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.5</a>	2.1
<a href="#">gi 40389047 gb AAR85701.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.5</a>	2.1
<a href="#">gi 22385227 gb AAM96144.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.1
<a href="#">gi 16517628 gb AAL24776.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.1
<a href="#">gi 13448300 gb AAK26973.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.1
<a href="#">gi 16517616 gb AAL24770.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.1
<a href="#">gi 7670925 gb AAF66282.1 </a>	polyprotein precursor [Hepatitis C ...	<a href="#">33.5</a>	2.1
<a href="#">gi 40389307 gb AAR85831.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.5</a>	2.1
<a href="#">gi 13448324 gb AAK26985.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.1
<a href="#">gi 4927618 gb AAD33195.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.1
<a href="#">gi 4469515 gb AAD21289.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.1
<a href="#">gi 16518642 gb AAL24922.1 </a>	glycoprotein [Hepatitis C virus] >...	<a href="#">33.5</a>	2.1
<a href="#">gi 4927567 gb AAD33144.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.1
<a href="#">gi 16517608 gb AAL24766.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.2
<a href="#">gi 13448302 gb AAK26974.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.2
<a href="#">gi 4927624 gb AAD33201.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.2
<a href="#">gi 4927612 gb AAD33189.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.2
<a href="#">gi 13448460 gb AAK27052.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.2
<a href="#">gi 4927602 gb AAD33179.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.2
<a href="#">gi 13448464 gb AAK27054.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.2
<a href="#">gi 13448437 gb AAK27041.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.2
<a href="#">gi 13448456 gb AAK27050.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">33.5</a>	2.2
<a href="#">gi 33413931 gb AAP55691.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.2

<a href="#">gi 7670869 gb AAF66254.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">33.5</a>	2.2
<a href="#">gi 32423840 gb AAP81306.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.3
<a href="#">gi 13448358 gb AAK27002.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.3
<a href="#">gi 4927601 gb AAD33178.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.3
<a href="#">gi 40389325 gb AAR85840.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.5</a>	2.3
<a href="#">gi 13448274 gb AAK26961.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.3
<a href="#">gi 16517624 gb AAL24774.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.3
<a href="#">gi 4927630 gb AAD33207.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.3
<a href="#">gi 4927571 gb AAD33148.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.3
<a href="#">gi 16517679 gb AAL24801.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.3
<a href="#">gi 33336845 gb AAQ13090.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 13448415 gb AAK27030.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 13448304 gb AAK26975.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 67810859 gb AAY82017.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 13448482 gb AAK27063.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 13448362 gb AAK27004.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 22385183 gb AAM96123.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">33.5</a>	2.4
<a href="#">gi 22385238 gb AAM96149.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 13448547 gb AAK27095.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 13448484 gb AAK27064.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 13448468 gb AAK27056.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 13448445 gb AAK27045.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 16517376 gb AAL24650.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 4927582 gb AAD33159.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.4
<a href="#">gi 67810864 gb AAY82019.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.5
<a href="#">gi 20339989 gb AAM19647.1 </a>	E1/E2 protein [Hepatitis C virus]	<a href="#">33.5</a>	2.5
<a href="#">gi 7670907 gb AAF66273.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">33.5</a>	2.5
<a href="#">gi 40389211 gb AAR85783.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.5</a>	2.5
<a href="#">gi 33637391 gb AAQ23851.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.5
<a href="#">gi 53801929 gb AAU94137.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.5
<a href="#">gi 40389407 gb AAR85881.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.5</a>	2.5
<a href="#">gi 40389299 gb AAR85827.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.5</a>	2.5
<a href="#">gi 40389139 gb AAR85747.1 </a>	E2 [Hepatitis C virus] >gi 4038913...	<a href="#">33.5</a>	2.5
<a href="#">gi 40389039 gb AAR85697.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.5</a>	2.5
<a href="#">gi 33337179 gb AAQ13257.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.5
<a href="#">gi 53802164 gb AAU94253.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.5
<a href="#">gi 7670875 gb AAF66257.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">33.5</a>	2.5
<a href="#">gi 13448470 gb AAK27057.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.6
<a href="#">gi 13448466 gb AAK27055.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.6
<a href="#">gi 16517630 gb AAL24777.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.6
<a href="#">gi 32423844 gb AAP81308.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">33.5</a>	2.6
<a href="#">gi 33337185 gb AAQ13260.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.6
<a href="#">gi 53801923 gb AAU94134.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.5</a>	2.6
<a href="#">gi 33337145 gb AAQ13240.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.6
<a href="#">gi 94322859 gb ABF17689.1 </a>	polyprotein precursor [Hepatitis C...	<a href="#">33.1</a>	2.6
<a href="#">gi 13448433 gb AAK27039.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.6
<a href="#">gi 53801921 gb AAU94133.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.6
<a href="#">gi 53801909 gb AAU94127.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.6
<a href="#">gi 13448506 gb AAK27075.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.7
<a href="#">gi 22385185 gb AAM96124.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.7
<a href="#">gi 30025526 gb AAP04377.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.7
<a href="#">gi 7728551 gb AAF68724.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.7
<a href="#">gi 53801724 gb AAU94035.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.7
<a href="#">gi 67810868 gb AAY82021.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.7
<a href="#">gi 53802168 gb AAU94255.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">33.1</a>	2.7
<a href="#">gi 67810857 gb AAY82016.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.7
<a href="#">gi 53802172 gb AAU94257.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.7
<a href="#">gi 53802170 gb AAU94256.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.7
<a href="#">gi 40389167 gb AAR85761.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.1</a>	2.8
<a href="#">gi 33336619 gb AAQ12977.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.8
<a href="#">gi 40389389 gb AAR85872.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.1</a>	2.8

<a href="#">gi 33336979 gb AAQ13157.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.8
<a href="#">gi 40389277 gb AAR85816.1 </a>	E2 [Hepatitis C virus] > <a href="#">gi 4038915...</a>	<a href="#">33.1</a>	2.8
<a href="#">gi 13448504 gb AAK27074.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.8
<a href="#">gi 20339825 gb AAM19566.1 </a>	E1/E2 protein [Hepatitis C virus]	<a href="#">33.1</a>	2.8
<a href="#">gi 20339823 gb AAM19565.1 </a>	E1/E2 protein [Hepatitis C virus]	<a href="#">33.1</a>	2.8
<a href="#">gi 13448486 gb AAK27065.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.8
<a href="#">gi 53802211 gb AAU94275.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.8
<a href="#">gi 93975 pir  S24082</a>	envelope protein - hepatitis C virus (fragm	<a href="#">33.1</a>	2.8
<a href="#">gi 33337229 gb AAQ13282.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.8
<a href="#">gi 33337163 gb AAQ13249.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.8
<a href="#">gi 13448298 gb AAK26972.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.9
<a href="#">gi 40389365 gb AAR85860.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.1</a>	2.9
<a href="#">gi 33337059 gb AAQ13197.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.9
<a href="#">gi 33336485 gb AAQ12910.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.9
<a href="#">gi 53801933 gb AAU94139.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	2.9
<a href="#">gi 56406528 gb AAV87613.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.0
<a href="#">gi 19569733 gb AAL92158.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.0
<a href="#">gi 13448494 gb AAK27069.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.0
<a href="#">gi 7649221 gb AAF65800.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">33.1</a>	3.0
<a href="#">gi 33336515 gb AAQ12925.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.0
<a href="#">gi 13448500 gb AAK27072.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.0
<a href="#">gi 33336937 gb AAQ13136.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.0
<a href="#">gi 16517374 gb AAL24649.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.0
<a href="#">gi 40389341 gb AAR85848.1 </a>	E2 [Hepatitis C virus] > <a href="#">gi 4038928...</a>	<a href="#">33.1</a>	3.1
<a href="#">gi 40389265 gb AAR85810.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.1</a>	3.1
<a href="#">gi 40389353 gb AAR85854.1 </a>	E2 [Hepatitis C virus] > <a href="#">gi 4038924...</a>	<a href="#">33.1</a>	3.1
<a href="#">gi 20339821 gb AAM19564.1 </a>	E1/E2 protein [Hepatitis C virus]	<a href="#">33.1</a>	3.1
<a href="#">gi 53801939 gb AAU94142.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.1
<a href="#">gi 40389415 gb AAR85885.1 </a>	E2 [Hepatitis C virus] > <a href="#">gi 4038941...</a>	<a href="#">33.1</a>	3.1
<a href="#">gi 33337167 gb AAQ13251.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.1
<a href="#">gi 33337249 gb AAQ13292.1 </a>	polyprotein [Hepatitis C virus] > <a href="#">g...</a>	<a href="#">33.1</a>	3.1
<a href="#">gi 13448270 gb AAK26959.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.2
<a href="#">gi 13448258 gb AAK26953.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.2
<a href="#">gi 37957175 gb AAP03917.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.2
<a href="#">gi 13448496 gb AAK27070.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.2
<a href="#">gi 13448488 gb AAK27066.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.2
<a href="#">gi 20339835 gb AAM19571.1 </a>	E1/E2 protein [Hepatitis C virus]	<a href="#">33.1</a>	3.2
<a href="#">gi 40389099 gb AAR85727.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.1</a>	3.3
<a href="#">gi 40389079 gb AAR85717.1 </a>	E2 [Hepatitis C virus]	<a href="#">33.1</a>	3.3
<a href="#">gi 37957171 gb AAP03915.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.3
<a href="#">gi 7649223 gb AAF65801.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">33.1</a>	3.3
<a href="#">gi 56406416 gb AAV87557.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.3
<a href="#">gi 13448276 gb AAK26962.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.3
<a href="#">gi 53802162 gb AAU94252.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.3
<a href="#">gi 32423860 gb AAP81316.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.3
<a href="#">gi 15866624 gb AAL10411.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.3
<a href="#">gi 7728977 gb AAF68775.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">33.1</a>	3.3
<a href="#">gi 52078280 gb AAU25900.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.4
<a href="#">gi 4927634 gb AAD33211.1 </a>	polyprotein [Hepatitis C virus] > <a href="#">gi...</a>	<a href="#">33.1</a>	3.4
<a href="#">gi 53802150 gb AAU94246.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">33.1</a>	3.4
<a href="#">gi 7728973 gb AAF68773.1 </a>	polyprotein precursor [Hepatitis C vir	<a href="#">32.7</a>	3.4
<a href="#">gi 25900865 dbj BAC41270.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.4
<a href="#">gi 7728555 gb AAF68726.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.4
<a href="#">gi 7728557 gb AAF68727.1 </a>	polyprotein [Hepatitis C virus] > <a href="#">gi...</a>	<a href="#">32.7</a>	3.4
<a href="#">gi 53802154 gb AAU94248.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.4
<a href="#">gi 53802152 gb AAU94247.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.4
<a href="#">gi 53802146 gb AAU94244.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.4
<a href="#">gi 33337231 gb AAQ13283.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.5
<a href="#">gi 53802160 gb AAU94251.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.5
<a href="#">gi 53802156 gb AAU94249.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.5
<a href="#">gi 53802148 gb AAU94245.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.5

<a href="#">gi 53801944 gb AAU94144.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.5
<a href="#">gi 40389379 gb AAR85867.1 </a>	E2 [Hepatitis C virus]	<a href="#">32.7</a>	3.6
<a href="#">gi 40389275 gb AAR85815.1 </a>	E2 [Hepatitis C virus]	<a href="#">32.7</a>	3.6
<a href="#">gi 40389261 gb AAR85808.1 </a>	E2 [Hepatitis C virus]	<a href="#">32.7</a>	3.6
<a href="#">gi 40389403 gb AAR85879.1 </a>	E2 [Hepatitis C virus] >gi 4038922...	<a href="#">32.7</a>	3.6
<a href="#">gi 22385174 gb AAM96119.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.6
<a href="#">gi 37957193 gb AAP03926.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.6
<a href="#">gi 33337223 gb AAQ13279.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.6
<a href="#">gi 13448268 gb AAK26958.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.6
<a href="#">gi 33337155 gb AAQ13245.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.7
<a href="#">gi 33337129 gb AAQ13232.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.7
<a href="#">gi 13448280 gb AAK26964.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.7
<a href="#">gi 37957177 gb AAP03918.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.7
<a href="#">gi 30025514 gb AAP04371.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.7
<a href="#">gi 20339829 gb AAM19568.1 </a>	E1/E2 protein [Hepatitis C virus]	<a href="#">32.7</a>	3.7
<a href="#">gi 53802158 gb AAU94250.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.7
<a href="#">gi 56406476 gb AAV87587.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.7
<a href="#">gi 32423866 gb AAP81319.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">32.7</a>	3.7
<a href="#">gi 4927581 gb AAD33158.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.7
<a href="#">gi 13448492 gb AAK27068.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.8
<a href="#">gi 13448236 gb AAK26942.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.8
<a href="#">gi 2580421 dbj BAA23132.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.8
<a href="#">gi 7728545 gb AAF68721.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.8
<a href="#">gi 13448254 gb AAK26951.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.8
<a href="#">gi 13448242 gb AAK26945.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.8
<a href="#">gi 33336693 gb AAQ13014.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.9
<a href="#">gi 33336685 gb AAQ13010.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.9
<a href="#">gi 33336689 gb AAQ13012.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">32.7</a>	3.9
<a href="#">gi 33336727 gb AAQ13031.1 </a>	polyprotein [Hepatitis C virus] >g...	<a href="#">32.7</a>	3.9
<a href="#">gi 33336597 gb AAQ12966.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.9
<a href="#">gi 22385233 gb AAM96147.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	3.9
<a href="#">gi 40389363 gb AAR85859.1 </a>	E2 [Hepatitis C virus]	<a href="#">32.7</a>	3.9
<a href="#">gi 40389287 gb AAR85821.1 </a>	E2 [Hepatitis C virus]	<a href="#">32.7</a>	3.9
<a href="#">gi 40389209 gb AAR85782.1 </a>	E2 [Hepatitis C virus]	<a href="#">32.7</a>	3.9
<a href="#">gi 51862090 gb AAU11697.1 </a>	envelope E1/E2 [Hepatitis C virus]...	<a href="#">32.7</a>	3.9
<a href="#">gi 33337189 gb AAQ13262.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">32.7</a>	4.0

## Alignments

Get selected sequences

Select all

Deselect all

Distance tree of results

> [gi|58198305|gb|AAW65860.1|](#) envelope protein [synthetic construct]  
Length=577

Score = 41.2 bits (95), Expect = 0.010, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G VSLF+PGAKQN  
Sbjct 221 GSAARTTTGLVSLFSPGAKQN 241

> [gi|64501453|gb|AAY41694.1|](#) envelope [Hepatitis C virus]  
Length=576

Score = 41.2 bits (95), Expect = 0.011, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21

GSAARTT+G VSLF+PGAKQN  
Sbjct 220 GSAARTTTGLVSLFSPGAKQN 240

> gi|58198313|gb|AAW65864.1| envelope protein [synthetic construct]  
Length=577

Score = 41.2 bits (95), Expect = 0.011, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G VSLF+PGAKQN  
Sbjct 221 GSAARTTTGLVSLFSPGAKQN 241

> gi|58198309|gb|AAW65862.1| envelope protein [synthetic construct]  
Length=577

Score = 41.2 bits (95), Expect = 0.011, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G VSLF+PGAKQN  
Sbjct 221 GSAARTTTGLVSLFSPGAKQN 241

> gi|64501451|gb|AAY41693.1| envelope [Hepatitis C virus]  
Length=576

Score = 41.2 bits (95), Expect = 0.011, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G VSLF+PGAKQN  
Sbjct 220 GSAARTTTGLVSLFSPGAKQN 240

> gi|64501435|gb|AAY41685.1| envelope [Hepatitis C virus]  
Length=576

Score = 41.2 bits (95), Expect = 0.012, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G VSLF+PGAKQN  
Sbjct 220 GSAARTTTGLVSLFSPGAKQN 240

> gi|58198311|gb|AAW65863.1| envelope protein [synthetic construct]  
Length=577

Score = 41.2 bits (95), Expect = 0.012, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G VSLF+PGAKQN  
Sbjct 221 GSAARTTTGLVSLFSPGAKQN 241

> gi|64501449|gb|AAY41692.1| envelope [Hepatitis C virus]

Length=576

Score = 41.2 bits (95), Expect = 0.012, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G VSLF+PGAKQN  
Sbjct 220 GSAARTTTGLVSLFSPGAKQN 240

> gi|64501447|gb|AAY41691.1| envelope [Hepatitis C virus]  
Length=576

Score = 41.2 bits (95), Expect = 0.012, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G VSLF+PGAKQN  
Sbjct 220 GSAARTTTGLVSLFSPGAKQN 240

> gi|2565261|gb|AAC61802.1| E2/NS1 protein [Hepatitis C virus]  
Length=364

Score = 39.7 bits (91), Expect = 0.030, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSG S FAPGAKQN  
Sbjct 13 GSAARTTSGITSFFAPGAKQN 33

> gi|15341438|gb|AAK95634.1| polyprotein [Hepatitis C virus]  
Length=335

Score = 39.7 bits (91), Expect = 0.031, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT GFV LF+PGAKQN  
Sbjct 199 GSAARTTGGFVGLFSPGAKQN 219

> gi|58220842|gb|AAW68049.1| envelope protein [synthetic construct]  
Length=607

Score = 39.3 bits (90), Expect = 0.037, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+GF SL +PGAKQN  
Sbjct 221 GSAARTTAGFASLLSPGAKQN 241

> gi|64501419|gb|AAY41677.1| envelope [Hepatitis C virus]  
gi|64501417|gb|AAY41676.1| envelope [Hepatitis C virus]  
Length=576

Score = 39.3 bits (90), Expect = 0.042, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+GF SL +PGAKQN  
Sbjct 220 GSAARTTAGFASLLSPGAKQN 240

> gi|64501423|gb|AAY41679.1| envelope [Hepatitis C virus]  
Length=576

Score = 39.3 bits (90), Expect = 0.044, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+GF SL +PGAKQN  
Sbjct 220 GSAARTTAGFASLLSPGAKQN 240

> gi|64501439|gb|AAY41687.1| envelope [Hepatitis C virus]  
Length=576

Score = 39.3 bits (90), Expect = 0.044, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAAR T+G VSLF+PGAKQN  
Sbjct 220 GSAARITTGLVSLFSPGAKQN 240

> gi|64501427|gb|AAY41681.1| envelope [Hepatitis C virus]  
Length=576

Score = 39.3 bits (90), Expect = 0.044, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAAR T+G VSLF+PGAKQN  
Sbjct 220 GSAARATTGLVSLFSPGAKQN 240

> gi|64501445|gb|AAY41690.1| envelope [Hepatitis C virus]  
Length=576

Score = 39.3 bits (90), Expect = 0.046, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAAR T+G VSLF+PGAKQN  
Sbjct 220 GSAARITTGLVSLFSPGAKQN 240

> gi|13448566|gb|AAK27104.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 38.1 bits (87), Expect = 0.099, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSG VSL +PGAKQN  
Sbjct 214 GSAARTTSGLVSLLLSPGAKQN 234

> gi|58198307|gb|AAW65861.1| envelope protein [synthetic construct]  
Length=577

Score = 37.7 bits (86), Expect = 0.13, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART G VSLF+PGAKQN  
Sbjct 221 GSAARTMIGLVSLFSPGAKQN 241

> gi|64501455|gb|AAV41695.1| envelope [Hepatitis C virus]  
Length=576

Score = 37.7 bits (86), Expect = 0.13, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART G VSLF+PGAKQN  
Sbjct 220 GSAARTMIGLVSLFSPGAKQN 240

> gi|64501429|gb|AAV41682.1| envelope [Hepatitis C virus]  
Length=576

Score = 37.7 bits (86), Expect = 0.14, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AAR T+G VSLF+PGAKQN  
Sbjct 220 GGAARATTGLVSLFSPGAKQN 240

> gi|33337015|gb|AAQ13175.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 37.0 bits (84), Expect = 0.20, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SGF SLF PGAKQN  
Sbjct 83 GSAGRTVSGFASLFTPGAKQN 103

> gi|64501425|gb|AAV41680.1| truncated envelope [Hepatitis C virus]  
gi|64501421|gb|AAV41678.1| truncated envelope [Hepatitis C virus]  
Length=249

Score = 37.0 bits (84), Expect = 0.20, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+GF SL +PGAKQN  
Sbjct 220 GSAARTTAGFASLLSPGAKQN 240

> gi|53801738|gb|AAU94042.1| polyprotein [Hepatitis C virus]  
gi|53801736|gb|AAU94041.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 37.0 bits (84), Expect = 0.21, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+AAR+TSGF+SLF PG+KQ+  
Sbjct 199 GTAARSTSGFISLFQPGSKQD 219

> gi|16518692|gb|AAL24947.1| glycoprotein [Hepatitis C virus]  
Length=85

Score = 37.0 bits (84), Expect = 0.23, Method: Composition-based stats.  
Identities = 19/21 (90%), Positives = 21/21 (100%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+GFVSLF+PGAKQN  
Sbjct 55 GSAARTTTGFVSLFSPGAKQN 75

> gi|13448510|gb|AAK27077.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 37.0 bits (84), Expect = 0.23, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSG+V+LF PGAKQ+  
Sbjct 214 GSAARTTSGWVNLFNPGAKQD 234

> gi|33337023|gb|AAQ13179.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.6 bits (83), Expect = 0.24, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SGF SLF PGAKQN  
Sbjct 83 GSAGRTVSGFASLFTPGAKQN 103

> gi|53801728|gb|AAU94037.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 36.6 bits (83), Expect = 0.25, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+AAR+TSGF+SLF PG+KQ+  
Sbjct 199 GTAARSTSGFISLFQPGSKQD 219

> gi|13448516|gb|AAK27080.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 36.6 bits (83), Expect = 0.25, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21

GSAARTTSG+V+LF PGAKQ+  
 Sbjct 214 GSAARTTSGWVNLFNPGAKQD 234

> gi|130455|sp|P26664|POLG\_HCV1 Genome polyprotein [Contains: Core protein p21 (Caps: C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]  
gi|329874|gb|AAA45676.1| HCV-1  
 Length=3011

Score = 36.6 bits (83), Expect = 0.26, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA T SGFVSL APGAKQN  
 Sbjct 390 GSAGHTVSGFVSLAPGAKQN 410

> gi|67810851|gb|AAY82013.1| polyprotein [Hepatitis C virus]  
 Length=1644

Score = 36.6 bits (83), Expect = 0.26, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAA+TT+G SLF+PGAKQN  
 Sbjct 390 GSAAKTTAGLTSFSPGAKQN 410

> gi|67810849|gb|AAY82012.1| polyprotein [Hepatitis C virus]  
 Length=1644

Score = 36.6 bits (83), Expect = 0.26, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAA+TT+G SLF+PGAKQN  
 Sbjct 390 GSAAKTTAGLTSFSPGAKQN 410

> gi|14532249|gb|AAK66556.1| HCV type 1a/1b chimera polyprotein [synthetic construct]  
gi|14532247|gb|AAK66555.1| HCV type 1a polyprotein [synthetic construct]  
gi|14532245|gb|AAK66554.1| HCV type 1a/1b chimera polyprotein [synthetic construct]  
 Length=3011

Score = 36.6 bits (83), Expect = 0.26, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA T SGFVSL APGAKQN  
 Sbjct 390 GSAGHTVSGFVSLAPGAKQN 410

> gi|14532251|gb|AAK66557.1| HCV type 1a/1b chimera mutant polyprotein [synthetic construct]  
 Length=3011

Score = 36.6 bits (83), Expect = 0.26, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 390 GSAGHTVSGFVSLAPGAKQN 410

> gi|53801732|gb|AAU94039.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 36.6 bits (83), Expect = 0.27, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+AAR+TSGF+SLF PG+KQ+  
Sbjct 199 GTAARSTSGFISLFQPGSKQD 219

> gi|33337057|gb|AAQ13196.1| polyprotein [Hepatitis C virus]

gi|33337055|gb|AAQ13195.1| polyprotein [Hepatitis C virus]  
gi|33337053|gb|AAQ13194.1| polyprotein [Hepatitis C virus]  
gi|33337051|gb|AAQ13193.1| polyprotein [Hepatitis C virus]  
gi|33337049|gb|AAQ13192.1| polyprotein [Hepatitis C virus]  
gi|33337047|gb|AAQ13191.1| polyprotein [Hepatitis C virus]  
gi|33337043|gb|AAQ13189.1| polyprotein [Hepatitis C virus]  
gi|33337041|gb|AAQ13188.1| polyprotein [Hepatitis C virus]  
gi|33337039|gb|AAQ13187.1| polyprotein [Hepatitis C virus]  
gi|33337037|gb|AAQ13186.1| polyprotein [Hepatitis C virus]  
gi|33337035|gb|AAQ13185.1| polyprotein [Hepatitis C virus]  
gi|33337029|gb|AAQ13182.1| polyprotein [Hepatitis C virus]  
gi|33337027|gb|AAQ13181.1| polyprotein [Hepatitis C virus]  
gi|33337019|gb|AAQ13177.1| polyprotein [Hepatitis C virus]  
gi|33337013|gb|AAQ13174.1| polyprotein [Hepatitis C virus]  
gi|33337011|gb|AAQ13173.1| polyprotein [Hepatitis C virus]  
gi|33337009|gb|AAQ13172.1| polyprotein [Hepatitis C virus]  
gi|33337007|gb|AAQ13171.1| polyprotein [Hepatitis C virus]  
gi|33337003|gb|AAQ13169.1| polyprotein [Hepatitis C virus]  
gi|33336999|gb|AAQ13167.1| polyprotein [Hepatitis C virus]

Length=115

Score = 36.6 bits (83), Expect = 0.28, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SGF SLF PGAKQN  
Sbjct 83 GSAGRTVSGFASLFTPGAKQN 103

> gi|37957242|gb|AAP03950.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.6 bits (83), Expect = 0.28, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 83 GSAGHTVSGFVSLAPGAKQN 103

> gi|436988|gb|AAA45601.1| putative  
Length=138

Score = 36.6 bits (83), Expect = 0.28, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA TTS GFVS F+PGAKQN  
Sbjct 22 GSAAHTTSGFVSFFSPGAKQN 42

> gi|7649227|gb|AAF65803.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 36.6 bits (83), Expect = 0.30, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +GF SLF+PGAKQN  
Sbjct 73 GSAARTAAGFASLFSPGAKQN 93

> gi|37957231|gb|AAP03945.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.2 bits (82), Expect = 0.32, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 83 GSAGHTVSGFVSL LAPGAKQN 103

> gi|33337017|gb|AAQ13176.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.2 bits (82), Expect = 0.32, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SGF SLF PGAKQN  
Sbjct 83 GSAGRTVSGFASLF TPGAKQN 103

> gi|33337005|gb|AAQ13170.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.2 bits (82), Expect = 0.32, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SGF SLF PGAKQN  
Sbjct 83 GSAGRTVSGFASLF PP GAKQN 103

> gi|67810855|gb|AAY82015.1| polyprotein [Hepatitis C virus]  
Length=1644

Score = 36.2 bits (82), Expect = 0.32, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAARTT+G LF+PGAKQN  
 Sbjct 390 GSAARTTAGLTGLFSPGAKQN 410

> gi|67810853|gb|AAY82014.1| polyprotein [Hepatitis C virus]  
 Length=1644

Score = 36.2 bits (82), Expect = 0.32, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAARTT+G LF+PGAKQN  
 Sbjct 390 GSAARTTAGLTGLFSPGAKQN 410

> gi|13448514|gb|AAK27079.1| polyprotein [Hepatitis C virus]  
 Length=326

Score = 36.2 bits (82), Expect = 0.33, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAARTTSG+V+LF PGAQ+  
 Sbjct 214 GSAARTTSGWVNLFNPGAQD 234

> gi|7670859|gb|AAF66249.1| polyprotein precursor [Hepatitis C virus]  
 Length=186

Score = 36.2 bits (82), Expect = 0.34, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAARTTSG V LF PGA+QN  
 Sbjct 73 GSAARTTSGLVGLFNPGAQQN 93

> gi|33336981|gb|AAQ13158.1| polyprotein [Hepatitis C virus]  
 Length=115

Score = 36.2 bits (82), Expect = 0.34, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA RT SGF SLF PGAKQN  
 Sbjct 83 GSAGRTVSGFASLFTPGAKQN 103

> gi|4469531|gb|AAD21305.1| polyprotein [Hepatitis C virus]  
 Length=326

Score = 36.2 bits (82), Expect = 0.34, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAAR TSGF +LF+PGAKQ+  
 Sbjct 214 GSAARATSGFANLFSPGAKQD 234

> gi|33337045|gb|AAQ13190.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.2 bits (82), Expect = 0.36, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SGF SLF PGAKQN  
Sbjct 83 GSAGRTVSGFASLFTPGAKQN 103

> gi|13448244|gb|AAK26946.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 36.2 bits (82), Expect = 0.36, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+TT+GFVSL +PG KQN  
Sbjct 214 GSAAKTTAGFVSLLSPPGPKQN 234

> gi|33337025|gb|AAQ13180.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.2 bits (82), Expect = 0.36, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SGF SLF PGAKQN  
Sbjct 83 GSAGRTVSGFASLFTPGAKQN 103

> gi|33337021|gb|AAQ13178.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.2 bits (82), Expect = 0.36, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SGF SLF PGAKQN  
Sbjct 83 GSAGRTVSGFASLFTPGAKQN 103

> gi|33336921|gb|AAQ13128.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.2 bits (82), Expect = 0.36, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGAKQN  
Sbjct 83 GSAGRTVSGLASLFTPGAKQN 103

> gi|53802198|gb|AAU94270.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 36.2 bits (82), Expect = 0.38, Method: Composition-based stats.

Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAAR+ SG S+FAPGAKQN  
Sbjct 199 GSAARSISGLTSIFAPGAKQN 219

> gi|13448555|gb|AAK27099.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 36.2 bits (82), Expect = 0.39, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART SG VSL +PGAKQN  
Sbjct 214 GSAARTASGLVSLSPGAKQN 234

> gi|33336927|gb|AAQ13131.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.2 bits (82), Expect = 0.39, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGAKQN  
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|37957251|gb|AAP03954.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.2 bits (82), Expect = 0.40, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 83 GSAGHTVSGFVSLAPGAKQN 103

> gi|37957229|gb|AAP03944.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 36.2 bits (82), Expect = 0.40, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 83 GSAGHTVSGFVSLAPGAKQN 103

> gi|33336925|gb|AAQ13130.1| polyprotein [Hepatitis C virus]  
gi|33336923|gb|AAQ13129.1| polyprotein [Hepatitis C virus]  
gi|33336919|gb|AAQ13127.1| polyprotein [Hepatitis C virus]  
gi|33336917|gb|AAQ13126.1| polyprotein [Hepatitis C virus]  
gi|33336915|gb|AAQ13125.1| polyprotein [Hepatitis C virus]  
gi|33336913|gb|AAQ13124.1| polyprotein [Hepatitis C virus]  
gi|33336911|gb|AAQ13123.1| polyprotein [Hepatitis C virus]  
gi|33336907|gb|AAQ13121.1| polyprotein [Hepatitis C virus]  
gi|33336905|gb|AAQ13120.1| polyprotein [Hepatitis C virus]

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gi|33336903|gb|AAQ13119.1| polyprotein [Hepatitis C virus]
gi|33336901|gb|AAQ13118.1| polyprotein [Hepatitis C virus]
gi|33336899|gb|AAQ13117.1| polyprotein [Hepatitis C virus]
gi|33336897|gb|AAQ13116.1| polyprotein [Hepatitis C virus]
gi|33336895|gb|AAQ13115.1| polyprotein [Hepatitis C virus]
gi|33336893|gb|AAQ13114.1| polyprotein [Hepatitis C virus]
gi|33336891|gb|AAQ13113.1| polyprotein [Hepatitis C virus]
gi|33336883|gb|AAQ13109.1| polyprotein [Hepatitis C virus]
gi|33336879|gb|AAQ13107.1| polyprotein [Hepatitis C virus]
gi|33336875|gb|AAQ13105.1| polyprotein [Hepatitis C virus]
gi|33336873|gb|AAQ13104.1| polyprotein [Hepatitis C virus]
gi|33336869|gb|AAQ13102.1| polyprotein [Hepatitis C virus]

```

Length=115

Score = 36.2 bits (82), Expect = 0.40, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

```

Query 1      GSAARTTSGFVSLFAPGAKQN  21
           GSA RT SG SLFAPGAKQN
Sbjct 83     GSAGRTVSGLASLFAPGAKQN 103

```

```

> gi|33336495|gb|AAQ12915.1| polyprotein [Hepatitis C virus]
Length=115

```

Score = 36.2 bits (82), Expect = 0.40, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

```

Query 1      GSAARTTSGFVSLFAPGAKQN  21
           GSA RT SG VSL APGAKQN
Sbjct 83     GSAGRTVSGLVSLAPGAKQN 103

```

```

> gi|33337001|gb|AAQ13168.1| polyprotein [Hepatitis C virus]
Length=115

```

Score = 35.8 bits (81), Expect = 0.40, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

```

Query 1      GSAARTTSGFVSLFAPGAKQN  21
           GSA RT SGF SLF PGAKQN
Sbjct 83     GSAGRTASGFASLFTPGAKQN 103

```

```

> gi|13344963|gb|AAK19135.1| polyprotein precursor [Hepatitis C virus]
Length=415

```

Score = 35.8 bits (81), Expect = 0.41, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

```

Query 1      GSAARTTSGFVSLFAPGAKQN  21
           GSA RT SGF SLF PGAKQN
Sbjct 390    GSAGRTVSGFASLFTPGAKQN 410

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> gi|7670871|gb|AAF66255.1| polyprotein precursor [Hepatitis C virus]
Length=186

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Score = 35.8 bits (81), Expect = 0.41, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAARTTSG V LF PGA+QN  
 Sbjct 73 GSAARTTSGLVGLFNPGAQQN 93

> gi|53802217|gb|AAU94278.1| polyprotein [Hepatitis C virus]  
 Length=426

Score = 35.8 bits (81), Expect = 0.41, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAAR+ SG S+FAPGAKQN  
 Sbjct 199 GSAARSISGLTSIFAPGAKQN 219

> gi|33336881|gb|AAQ13108.1| polyprotein [Hepatitis C virus]  
 Length=115

Score = 35.8 bits (81), Expect = 0.41, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA RT SG SLFAPGAKQN  
 Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|37957244|gb|AAP03951.1| polyprotein [Hepatitis C virus]  
 Length=115

Score = 35.8 bits (81), Expect = 0.41, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA T SGFVSL APGAKQN  
 Sbjct 83 GSAGHTVSGFVSLLAPGAKQN 103

> gi|37957239|gb|AAP03949.1| polyprotein [Hepatitis C virus]

gi|37957237|gb|AAP03948.1| polyprotein [Hepatitis C virus]  
gi|37957235|gb|AAP03947.1| polyprotein [Hepatitis C virus]  
gi|37957227|gb|AAP03943.1| polyprotein [Hepatitis C virus]  
gi|37957225|gb|AAP03942.1| polyprotein [Hepatitis C virus]  
gi|37957223|gb|AAP03941.1| polyprotein [Hepatitis C virus]  
gi|37957221|gb|AAP03940.1| polyprotein [Hepatitis C virus]  
gi|37957219|gb|AAP03939.1| polyprotein [Hepatitis C virus]  
gi|37957217|gb|AAP03938.1| polyprotein [Hepatitis C virus]  
gi|37957215|gb|AAP03937.1| polyprotein [Hepatitis C virus]  
gi|37957213|gb|AAP03936.1| polyprotein [Hepatitis C virus]  
gi|37957211|gb|AAP03935.1| polyprotein [Hepatitis C virus]  
gi|37957209|gb|AAP03934.1| polyprotein [Hepatitis C virus]  
gi|37957207|gb|AAP03933.1| polyprotein [Hepatitis C virus]  
gi|37957205|gb|AAP03932.1| polyprotein [Hepatitis C virus]  
gi|37957203|gb|AAP03931.1| polyprotein [Hepatitis C virus]  
gi|37957201|gb|AAP03930.1| polyprotein [Hepatitis C virus]  
gi|37957199|gb|AAP03929.1| polyprotein [Hepatitis C virus]  
gi|37957195|gb|AAP03927.1| polyprotein [Hepatitis C virus]

Length=115

Score = 35.8 bits (81), Expect = 0.42, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 83 GSAGHTVSGFVSLAPGAKQN 103

> gi|33336889|gb|AAQ13112.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.8 bits (81), Expect = 0.42, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGAKQN  
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|13448238|gb|AAK26943.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 35.8 bits (81), Expect = 0.42, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+TT+GFVSL +PG KQN  
Sbjct 214 GSAAKTTAGFVSLSPGPKQN 234

> gi|7670919|gb|AAF66279.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 35.8 bits (81), Expect = 0.42, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSG V LF PGA+QN  
Sbjct 73 GSAARTTSGLVGLFNPGAQQN 93

> gi|7670867|gb|AAF66253.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 35.8 bits (81), Expect = 0.42, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSG V LF PGA+QN  
Sbjct 73 GSAARTTSGLVGLFNPGAQQN 93

> gi|33336867|gb|AAQ13101.1| polyprotein [Hepatitis C virus]  
gi|33336803|gb|AAQ13069.1| polyprotein [Hepatitis C virus]  
gi|33336791|gb|AAQ13063.1| polyprotein [Hepatitis C virus]  
gi|33336777|gb|AAQ13056.1| polyprotein [Hepatitis C virus]  
gi|33336775|gb|AAQ13055.1| polyprotein [Hepatitis C virus]  
gi|33336771|gb|AAQ13053.1| polyprotein [Hepatitis C virus]  
gi|33336769|gb|AAQ13052.1| polyprotein [Hepatitis C virus]  
gi|33336767|gb|AAQ13051.1| polyprotein [Hepatitis C virus]

gi|33336765|gb|AAQ13050.1| polyprotein [Hepatitis C virus]  
 gi|33336757|gb|AAQ13046.1| polyprotein [Hepatitis C virus]  
 gi|33336751|gb|AAQ13043.1| polyprotein [Hepatitis C virus]  
 gi|33336747|gb|AAQ13041.1| polyprotein [Hepatitis C virus]  
 Length=115

Score = 35.8 bits (81), Expect = 0.43, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA RT SG SLFAPGAKQN  
 Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|33336885|gb|AAQ13110.1| polyprotein [Hepatitis C virus]  
 Length=115

Score = 35.8 bits (81), Expect = 0.44, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA RT SG SLFAPGAKQN  
 Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|16518684|gb|AAL24943.1| glycoprotein [Hepatitis C virus]  
 Length=85

Score = 35.8 bits (81), Expect = 0.44, Method: Composition-based stats.  
 Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAARTT+G VSLF+PGAKQN  
 Sbjct 55 GSAARTTTGLVSLFSPGAKQN 75

> gi|7670861|gb|AAF66250.1| polyprotein precursor [Hepatitis C virus]  
 Length=186

Score = 35.8 bits (81), Expect = 0.44, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAARTTSG V LF PGA+QN  
 Sbjct 73 GSAARTTSGLVGLFNPGAQQN 93

> gi|7670939|gb|AAF66289.1| polyprotein precursor [Hepatitis C virus]  
 Length=186

Score = 35.8 bits (81), Expect = 0.45, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAARTTSG V LF PGA+QN  
 Sbjct 73 GSAARTTSGLVGLFNPGAQQN 93

> gi|33336909|gb|AAQ13122.1| polyprotein [Hepatitis C virus]  
 Length=115

Score = 35.8 bits (81), Expect = 0.47, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGAKQN  
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|4927491|gb|AAD33137.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 35.8 bits (81), Expect = 0.47, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G SLF+PGAKQN  
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|37957257|gb|AAP03957.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.8 bits (81), Expect = 0.48, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 83 GSAGHTVSGFVSLAPGAKQN 103

> gi|13448474|gb|AAK27059.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 35.8 bits (81), Expect = 0.49, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA T+GF LFAPGAKQN  
Sbjct 214 GSAAHATAGFAGLFAPGAKQN 234

> gi|37957255|gb|AAP03956.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.8 bits (81), Expect = 0.50, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 83 GSAGHTVSGFVSLAPGAKQN 103

> gi|13448502|gb|AAK27073.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 35.8 bits (81), Expect = 0.50, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21

GSAA T+GF SLF+PGAKQN  
Sbjct 214 GSAAHATAGFASLFSPGAKQN 234

> gi|37957179|gb|AAP03919.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.8 bits (81), Expect = 0.50, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSG LF PGAKQN  
Sbjct 83 GSAARTTSGLAGLFTPGAKQN 103

> gi|13448524|gb|AAK27084.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 35.8 bits (81), Expect = 0.51, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GS ARTTSGF + F PGAKQN  
Sbjct 214 GSVARTTSGFANFFNPGAKQN 234

> gi|37957249|gb|AAP03953.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.8 bits (81), Expect = 0.52, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 83 GSAGHTVSGFVSL LAPGAKQN 103

> gi|37957246|gb|AAP03952.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.8 bits (81), Expect = 0.52, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 83 GSAGHTVSGFVSL LAPGAKQN 103

> gi|33336887|gb|AAQ13111.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.8 bits (81), Expect = 0.52, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGAKQN  
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|53801742|gb|AAU94044.1| polyprotein [Hepatitis C virus]

Length=426

Score = 35.8 bits (81), Expect = 0.52, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AAR+TSGF+SLF PG+KQ+  
Sbjct 199 GVAARSTSGFISLFQPGSKQD 219

> gi|4927589|gb|AAD33166.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 35.4 bits (80), Expect = 0.55, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +GF SLF+PGAKQN  
Sbjct 65 GSAARTAAGFASLFSPGAKQN 85

> gi|4927496|gb|AAD33142.1| polyprotein [Hepatitis C virus]  
gi|4927495|gb|AAD33141.1| polyprotein [Hepatitis C virus]  
gi|4927494|gb|AAD33140.1| polyprotein [Hepatitis C virus]  
gi|4927493|gb|AAD33139.1| polyprotein [Hepatitis C virus]  
gi|4927492|gb|AAD33138.1| polyprotein [Hepatitis C virus]  
gi|4927490|gb|AAD33136.1| polyprotein [Hepatitis C virus]  
gi|4927489|gb|AAD33135.1| polyprotein [Hepatitis C virus]  
gi|4927488|gb|AAD33134.1| polyprotein [Hepatitis C virus]  
gi|4927487|gb|AAD33133.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 35.4 bits (80), Expect = 0.55, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G SLF+PGAKQN  
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|53801730|gb|AAU94038.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 35.4 bits (80), Expect = 0.55, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AAR+TSGF+SLF PG+KQ+  
Sbjct 199 GVAARSTSGFISLFQPGSKQD 219

> gi|51558189|gb|AAU06654.1| envelope glycoprotein [Hepatitis C virus]  
Length=126

Score = 35.4 bits (80), Expect = 0.56, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+AARTTSGF SLF PGAKQN  
Sbjct 9 GAAARTTSGFTSLFRPGAKQN 29

> gi|53801726|gb|AAU94036.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 35.4 bits (80), Expect = 0.56, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AAR+TSGF+SLF PG+KQ+  
Sbjct 199 GVAARSTSGFISLFQPGSKQD 219

> gi|53801734|gb|AAU94040.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 35.4 bits (80), Expect = 0.57, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AAR+TSGF+SLF PG+KQ+  
Sbjct 199 GVAARSTSGFISLFQPGSKQD 219

> gi|33336863|gb|AAQ13099.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.4 bits (80), Expect = 0.57, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGA+QN  
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|38539525|gb|AAR23635.1| polyprotein [Hepatitis C virus]  
Length=184

Score = 35.4 bits (80), Expect = 0.58, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+TT+G VSLF PGAKQN  
Sbjct 68 GSAAQTTAGLVSLFKPGAKQN 88

> gi|221688|dbj|BAA14118.1| X protein [Hepatitis C virus]  
Length=129

Score = 35.4 bits (80), Expect = 0.58, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 72 GSAGHTVSGFVSLAPGAKQN 92

> gi|37957233|gb|AAP03946.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.4 bits (80), Expect = 0.59, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SGFVSL APGAKQN  
Sbjct 83 GSAGHTVSGFVSLAPGAKQN 103

> gi|53801718|gb|AAU94032.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 35.4 bits (80), Expect = 0.59, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AAR+TSGF+SLF PG+KQ+  
Sbjct 199 GVAARSTSGFISLFQPGSKQD 219

> gi|33336821|gb|AAQ13078.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.4 bits (80), Expect = 0.59, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA+RT SG SLFAPGA+QN  
Sbjct 83 GSASRTVSGLASLFAPGARQN 103

> gi|4927621|gb|AAD33198.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 35.4 bits (80), Expect = 0.60, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G SLF+PGAKQN  
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|4927579|gb|AAD33156.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 35.4 bits (80), Expect = 0.63, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G SLF+PGAKQN  
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|33336839|gb|AAQ13087.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.4 bits (80), Expect = 0.64, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGA+QN

Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|7670905|gb|AAF66272.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 35.4 bits (80), Expect = 0.64, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSG V LF PGA+QN  
Sbjct 73 GSAARTTSGLVGLFNPGAQQN 93

> gi|13448551|gb|AAK27097.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 35.4 bits (80), Expect = 0.66, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GS ARTTSGF + F PGAKQN  
Sbjct 214 GSIARTTSGFANFFDPGAKQN 234

> gi|13344959|gb|AAK19133.1| polyprotein precursor [Hepatitis C virus]  
Length=415

Score = 35.4 bits (80), Expect = 0.66, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGAKQN  
Sbjct 390 GSAGRTVSGLASLFAPGAKQN 410

> gi|33336865|gb|AAQ13100.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.4 bits (80), Expect = 0.66, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGA+QN  
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|16518694|gb|AAL24948.1| glycoprotein [Hepatitis C virus]  
gi|16518690|gb|AAL24946.1| glycoprotein [Hepatitis C virus]  
gi|16518688|gb|AAL24945.1| glycoprotein [Hepatitis C virus]  
gi|16518686|gb|AAL24944.1| glycoprotein [Hepatitis C virus]  
Length=85

Score = 35.4 bits (80), Expect = 0.67, Method: Composition-based stats.  
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G VSLF+PGAKQN  
Sbjct 55 GSAARTTTGLVSLFSPGAKQN 75

> gi|13448545|gb|AAK27094.1| polyprotein [Hepatitis C virus]  
gi|13448543|gb|AAK27093.1| polyprotein [Hepatitis C virus]  
 Length=326

Score = 35.4 bits (80), Expect = 0.67, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GS ARTTSGF + F PGAKQN  
 Sbjct 214 GSIARTTSGFANFFDPGAKQN 234

> gi|13448541|gb|AAK27092.1| polyprotein [Hepatitis C virus]  
 Length=326

Score = 35.4 bits (80), Expect = 0.67, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GS ARTTSGF + F PGAKQN  
 Sbjct 214 GSIARTTSGFANFFNPGAKQN 234

> gi|33336851|gb|AAQ13093.1| polyprotein [Hepatitis C virus]  
 Length=115

Score = 35.0 bits (79), Expect = 0.70, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA RT SG SLFAPGA+QN  
 Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|13448539|gb|AAK27091.1| polyprotein [Hepatitis C virus]  
 Length=326

Score = 35.0 bits (79), Expect = 0.71, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GS ARTTSGF + F PGAKQN  
 Sbjct 214 GSIARTTSGFANFFDPGAKQN 234

> gi|33336931|gb|AAQ13133.1| polyprotein [Hepatitis C virus]  
gi|33336871|gb|AAQ13103.1| polyprotein [Hepatitis C virus]  
 Length=115

Score = 35.0 bits (79), Expect = 0.71, Method: Composition-based stats.  
 Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA RT SG SLFAPGAKQN  
 Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|4927584|gb|AAD33161.1| polyprotein [Hepatitis C virus]  
 Length=175

Score = 35.0 bits (79), Expect = 0.71, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G SLF+PGAKQN  
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|4927575|gb|AAD33152.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 35.0 bits (79), Expect = 0.71, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+G SLF+PGAKQN  
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|53801809|gb|AAU94077.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 35.0 bits (79), Expect = 0.72, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+AAR+T+ FVSL APGA+QN  
Sbjct 199 GTAARSTASFVSL LAPGARQN 219

> gi|53801937|gb|AAU94141.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 35.0 bits (79), Expect = 0.73, Method: Composition-based stats.  
Identities = 15/20 (75%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20  
G+AAR T+GFVS F+PGAKQ  
Sbjct 199 GTAARDTAGFVSFFSPGAKQ 218

> gi|221587|dbj|BAA01582.1| polyprotein precursor [Hepatitis C virus]  
Length=3011

Score = 35.0 bits (79), Expect = 0.76, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AAR SG VSLF PGAKQN  
Sbjct 390 GQAARAMSGLVSLFTPGAKQN 410

> gi|13448316|gb|AAK26981.1| polyprotein [Hepatitis C virus]  
gi|13448310|gb|AAK26978.1| polyprotein [Hepatitis C virus]  
gi|13448308|gb|AAK26977.1| polyprotein [Hepatitis C virus]  
gi|13448306|gb|AAK26976.1| polyprotein [Hepatitis C virus]  
Length=327

Score = 35.0 bits (79), Expect = 0.77, Method: Composition-based stats.

Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+ +RTTSGFV L +PGAKQN  
Sbjct 215 GAVSRTTSGFVGLLSPGAKQN 235

> gi|33336823|gb|AAQ13079.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.0 bits (79), Expect = 0.77, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGA+QN  
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|13448620|gb|AAK27131.1| polyprotein [Hepatitis C virus]  
Length=323

Score = 35.0 bits (79), Expect = 0.77, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSGFV L PG+KQ+  
Sbjct 211 GSAARTTSGFVGLLNPGSKQD 231

> gi|33336861|gb|AAQ13098.1| polyprotein [Hepatitis C virus]  
gi|33336857|gb|AAQ13096.1| polyprotein [Hepatitis C virus]  
gi|33336855|gb|AAQ13095.1| polyprotein [Hepatitis C virus]  
gi|33336853|gb|AAQ13094.1| polyprotein [Hepatitis C virus]  
gi|33336849|gb|AAQ13092.1| polyprotein [Hepatitis C virus]  
gi|33336847|gb|AAQ13091.1| polyprotein [Hepatitis C virus]  
gi|33336843|gb|AAQ13089.1| polyprotein [Hepatitis C virus]  
gi|33336841|gb|AAQ13088.1| polyprotein [Hepatitis C virus]  
gi|33336837|gb|AAQ13086.1| polyprotein [Hepatitis C virus]  
gi|33336835|gb|AAQ13085.1| polyprotein [Hepatitis C virus]  
gi|33336833|gb|AAQ13084.1| polyprotein [Hepatitis C virus]  
gi|33336829|gb|AAQ13082.1| polyprotein [Hepatitis C virus]  
gi|33336827|gb|AAQ13081.1| polyprotein [Hepatitis C virus]  
gi|33336825|gb|AAQ13080.1| polyprotein [Hepatitis C virus]  
gi|33336813|gb|AAQ13074.1| polyprotein [Hepatitis C virus]  
gi|33336811|gb|AAQ13073.1| polyprotein [Hepatitis C virus]  
gi|33336809|gb|AAQ13072.1| polyprotein [Hepatitis C virus]  
gi|33336807|gb|AAQ13071.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.0 bits (79), Expect = 0.79, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGA+QN  
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|53801951|gb|AAU94147.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 35.0 bits (79), Expect = 0.79, Method: Composition-based stats.  
Identities = 15/20 (75%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20  
G+AAR T+GFVS F+PGAKQ  
Sbjct 199 GTAARDTAGFVSFFSPGAKQ 218

> gi|13448549|gb|AAK27096.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 35.0 bits (79), Expect = 0.80, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GS ARTTSGF + F PGAKQN  
Sbjct 214 GSIARTTSGFANFFDPGAKQN 234

> gi|13448320|gb|AAK26983.1| polyprotein [Hepatitis C virus]  
Length=327

Score = 35.0 bits (79), Expect = 0.80, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+ +RTTSGFV L +PGAKQN  
Sbjct 215 GAVSRRTSGFVGLLSPGAKQN 235

> gi|13448588|gb|AAK27115.1| polyprotein [Hepatitis C virus]  
gi|13448586|gb|AAK27114.1| polyprotein [Hepatitis C virus]  
gi|13448584|gb|AAK27113.1| polyprotein [Hepatitis C virus]  
gi|13448582|gb|AAK27112.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 35.0 bits (79), Expect = 0.81, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+TT G VSLF PGAKQN  
Sbjct 214 GSAAQTTLGLVSLFRPGAKQN 234

> gi|53802206|gb|AAU94273.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 35.0 bits (79), Expect = 0.81, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+ T GF SLF+PGA+QN  
Sbjct 199 GSAAKITQGFSSSLFSPGARQN 219

> gi|89519415|gb|ABD75829.1| polyprotein [Hepatitis C virus]  
Length=3008

Score = 35.0 bits (79), Expect = 0.81, Method: Composition-based stats.  
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20  
GSAA+TTSG VS+FAPGA Q  
Sbjct 390 GSAAQTTSGLVSMFAPGASQ 409

> gi|33336965|gb|AAQ13150.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.0 bits (79), Expect = 0.82, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLF PGAKQN  
Sbjct 83 GSAGRTVSGLASLFTPGAKQN 103

> gi|13448326|gb|AAK26986.1| polyprotein [Hepatitis C virus]  
Length=327

Score = 35.0 bits (79), Expect = 0.82, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+ +RTTSGFV L +PGAKQN  
Sbjct 215 GAVSRRTSGFVGLLSPGAKQN 235

> gi|33337033|gb|AAQ13184.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.0 bits (79), Expect = 0.83, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT GF SLF PGAKQN  
Sbjct 83 GSAGRTVPGFASLFTPGAKQN 103

> gi|13448314|gb|AAK26980.1| polyprotein [Hepatitis C virus]  
Length=327

Score = 35.0 bits (79), Expect = 0.84, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+ +RTTSGFV L +PGAKQN  
Sbjct 215 GAVSRRTSGFVGLLSPGAKQN 235

> gi|56406500|gb|AAV87599.1| polyprotein [Hepatitis C virus]  
Length=179

Score = 35.0 bits (79), Expect = 0.85, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSG V +F PGA+QN  
Sbjct 62 GSAARTTSGVVGIFTPGAQQN 82

> gi|33336761|gb|AAQ13048.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.0 bits (79), Expect = 0.85, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG V L APGAKQN  
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|13448578|gb|AAK27110.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 35.0 bits (79), Expect = 0.86, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+TT G VSLF PGAKQN  
Sbjct 214 GSAAQTTLGLVSLFRPGAKQN 234

> gi|33637194|gb|AAQ23753.1| polyprotein [Hepatitis C virus]  
Length=190

Score = 35.0 bits (79), Expect = 0.86, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA R+T+GF LF+PGAKQN  
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|33336525|gb|AAQ12930.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.0 bits (79), Expect = 0.87, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG V L APGAKQN  
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|13448322|gb|AAK26984.1| polyprotein [Hepatitis C virus]  
Length=327

Score = 35.0 bits (79), Expect = 0.87, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+ +RTTSGFV L +PGAKQN  
Sbjct 215 GAVSRRTSGFVGLLSPGAKQN 235

> gi|33336639|gb|AAQ12987.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.0 bits (79), Expect = 0.89, Method: Composition-based stats.

Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG LFAPGAKQN  
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|13448318|gb|AAK26982.1| polyprotein [Hepatitis C virus]  
Length=327

Score = 35.0 bits (79), Expect = 0.89, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+ +RTTSGFV L +PGAKQN  
Sbjct 215 GAVSRTTSGFVGLLSPGAKQN 235

> gi|53801935|gb|AAU94140.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 35.0 bits (79), Expect = 0.89, Method: Composition-based stats.  
Identities = 15/20 (75%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20  
G+AAR T+GFVS F+PGAKQ  
Sbjct 199 GTAARDTAGFVSFFSPGAKQ 218

> gi|33336815|gb|AAQ13075.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 35.0 bits (79), Expect = 0.89, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGA+QN  
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|7649241|gb|AAF65810.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 34.7 bits (78), Expect = 0.90, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|109259768|gb|AAW65879.2| envelope protein [synthetic construct]  
Length=578

Score = 34.7 bits (78), Expect = 0.90, Method: Composition-based stats.  
Identities = 14/21 (66%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+A R T+GF LF PGAKQN  
Sbjct 221 GTAGRATAGFTEFTPAGAKQN 241

> gi|13448296|gb|AAK26971.1| polyprotein [Hepatitis C virus]  
Length=327

Score = 34.7 bits (78), Expect = 0.91, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G A+RTTSG SL APGAKQN  
Sbjct 215 GVASRTTSGLASLLAPGAKQN 235

> gi|13448294|gb|AAK26970.1| polyprotein [Hepatitis C virus]  
Length=327

Score = 34.7 bits (78), Expect = 0.91, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G A+RTTSG SL APGAKQN  
Sbjct 215 GVASRTTSGLASLLAPGAKQN 235

> gi|53801948|gb|AAU94146.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 34.7 bits (78), Expect = 0.91, Method: Composition-based stats.  
Identities = 15/20 (75%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20  
G+AAR T+GFVS F+PGAKQ  
Sbjct 199 GTAARDTAGFVSFFSPGAKQ 218

> gi|26053623|ref|NP\_751921.1| **G** E2 protein; viral envelope protein [Hepatitis C virus]  
Length=363

Score = 34.7 bits (78), Expect = 0.91, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RTT+G V L PGAKQN  
Sbjct 7 GSAGRRTAGLVGLLTPGAKQN 27

> gi|13448580|gb|AAK27111.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 34.7 bits (78), Expect = 0.92, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+TT G VSLF PGAKQN  
Sbjct 214 GSAAQTTLGLVSLFRPGAKQN 234

> gi|64501433|gb|AAY41684.1| envelope [Hepatitis C virus]  
Length=576

Score = 34.7 bits (78), Expect = 0.92, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAAR T+G SL +PGAKQN  
Sbjct 220 GSAARITAGIASLLSPGAKQN 240

> gi|37957282|gb|AAP03969.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.7 bits (78), Expect = 0.92, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GS ARTT+G SLF PGAKQN  
Sbjct 83 GSVARTTAGLTSLFTPGAKQN 103

> gi|58198303|gb|AAW65859.1| envelope protein [synthetic construct]  
Length=577

Score = 34.7 bits (78), Expect = 0.93, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAAR T+G SL +PGAKQN  
Sbjct 221 GSAARITAGIASLLSPGAKQN 241

> gi|33336957|gb|AAQ13146.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.7 bits (78), Expect = 0.95, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLF PGAKQN  
Sbjct 83 GSAGRTVSGLASLFTPGAKQN 103

> gi|7649243|gb|AAF65811.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 34.7 bits (78), Expect = 0.96, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|109259770|gb|AAW65880.2| envelope protein [synthetic construct]  
Length=578

Score = 34.7 bits (78), Expect = 0.98, Method: Composition-based stats.  
Identities = 14/21 (66%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+A R T+GF LF PGAKQN

Sbjct 221 GTAGRATAGFTELFPGAKQN 241

> gi|64501431|gb|AAY41683.1| envelope [Hepatitis C virus]  
Length=576

Score = 34.7 bits (78), Expect = 0.98, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAAR T+G SL +PGAKQN  
Sbjct 220 GSAARITAGIASLLSPGAKQN 240

> gi|33336563|gb|AAQ12949.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.7 bits (78), Expect = 0.99, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG LFAPGAKQN  
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|7649239|gb|AAF65809.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 34.7 bits (78), Expect = 0.99, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|7649247|gb|AAF65813.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|94317855|gb|ABF15187.1| polyprotein precursor [Hepatitis C virus]  
Length=176

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G A RTTSG VSLF PG+KQN  
Sbjct 68 GQAGRTTSGLVSLFKPGSKQN 88

> gi|7670903|gb|AAF66271.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSG V LF PGA+ N  
Sbjct 73 GSAARTTSGLVGLFNPGAQHN 93

> gi|64501443|gb|AAY41689.1| envelope [Hepatitis C virus]  
Length=576

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAAR T+G SL +PGAKQN  
Sbjct 220 GSAARITAGIASLLSPGAKQN 240

> gi|33336997|gb|AAQ13166.1| polyprotein [Hepatitis C virus]

gi|33336995|gb|AAQ13165.1| polyprotein [Hepatitis C virus]  
gi|33336993|gb|AAQ13164.1| polyprotein [Hepatitis C virus]  
gi|33336991|gb|AAQ13163.1| polyprotein [Hepatitis C virus]  
gi|33336989|gb|AAQ13162.1| polyprotein [Hepatitis C virus]  
gi|33336987|gb|AAQ13161.1| polyprotein [Hepatitis C virus]  
gi|33336985|gb|AAQ13160.1| polyprotein [Hepatitis C virus]  
gi|33336977|gb|AAQ13156.1| polyprotein [Hepatitis C virus]  
gi|33336975|gb|AAQ13155.1| polyprotein [Hepatitis C virus]  
gi|33336971|gb|AAQ13153.1| polyprotein [Hepatitis C virus]  
gi|33336969|gb|AAQ13152.1| polyprotein [Hepatitis C virus]  
gi|33336967|gb|AAQ13151.1| polyprotein [Hepatitis C virus]  
gi|33336963|gb|AAQ13149.1| polyprotein [Hepatitis C virus]  
gi|33336961|gb|AAQ13148.1| polyprotein [Hepatitis C virus]  
gi|33336959|gb|AAQ13147.1| polyprotein [Hepatitis C virus]  
gi|33336955|gb|AAQ13145.1| polyprotein [Hepatitis C virus]  
gi|33336953|gb|AAQ13144.1| polyprotein [Hepatitis C virus]  
gi|33336951|gb|AAQ13143.1| polyprotein [Hepatitis C virus]  
gi|33336949|gb|AAQ13142.1| polyprotein [Hepatitis C virus]  
gi|33336947|gb|AAQ13141.1| polyprotein [Hepatitis C virus]  
gi|33336943|gb|AAQ13139.1| polyprotein [Hepatitis C virus]  
gi|33336941|gb|AAQ13138.1| polyprotein [Hepatitis C virus]  
gi|33336939|gb|AAQ13137.1| polyprotein [Hepatitis C virus]  
gi|33336935|gb|AAQ13135.1| polyprotein [Hepatitis C virus]  
gi|33336933|gb|AAQ13134.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLF PGAKQN  
Sbjct 83 GSAGRTVSGLASLFTPGAKQN 103

> gi|7649237|gb|AAF65808.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAART +G SLF+PGAKQN  
 Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|33336507|gb|AAQ12921.1| polyprotein [Hepatitis C virus]  
 Length=115

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA T SG VSL APGAKQN  
 Sbjct 83 GSAGHTVSGLVSL LAPGAKQN 103

> gi|4469530|gb|AAD21304.1| polyprotein [Hepatitis C virus]  
 Length=326

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
 Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 G AAR TSGF +LF+PGAKQ+  
 Sbjct 214 GGAARATSGFANLFSPGAKQD 234

> gi|50235322|gb|AAT69968.1| polyprotein [Hepatitis C virus]  
 Length=3011

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
 Identities = 14/21 (66%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA R+T+G V LF+PGA+QN  
 Sbjct 390 GSAGRSTAGLVGLFSPGARQN 410

> gi|33637202|gb|AAQ23757.1| polyprotein [Hepatitis C virus]  
 Length=190

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
 Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA R+T+GF LF+PGAKQN  
 Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|7649233|gb|AAF65806.1| polyprotein precursor [Hepatitis C virus]  
gi|7649231|gb|AAF65805.1| polyprotein precursor [Hepatitis C virus]  
gi|7649225|gb|AAF65802.1| polyprotein precursor [Hepatitis C virus]  
 Length=186

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAART +G SLF+PGAKQN

Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|33637208|gb|AAQ23760.1| polyprotein [Hepatitis C virus]  
Length=189

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA R+T+GF LF+PGAKQN  
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|7670911|gb|AAF66275.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTS V LF PGA+QN  
Sbjct 73 GSAARTTSSLVGLFNPGAQQN 93

> gi|7670863|gb|AAF66251.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTS V LF PGA+QN  
Sbjct 73 GSAARTTSSLVGLFNPGAQQN 93

> gi|53801865|gb|AAU94105.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA T SG ++FAPGAKQN  
Sbjct 199 GSAAHTVSGLATIFAPGAKQN 219

> gi|13448285|gb|AAK26966.1| polyprotein [Hepatitis C virus]  
Length=327

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+ +RTTSGF L APGAKQN  
Sbjct 215 GAVSRTTSGFAGLLAPGAKQN 235

> gi|7649235|gb|AAF65807.1| polyprotein precursor [Hepatitis C virus]  
gi|7649229|gb|AAF65804.1| polyprotein precursor [Hepatitis C virus]

Length=186

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|4927576|gb|AAD33153.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+AAARTT+G SLF+PGAKQN  
Sbjct 65 GTAARTTAGLASLFSPGAKQN 85

> gi|33336831|gb|AAQ13083.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGA+QN  
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|33336779|gb|AAQ13057.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA+ T SG VSL APGAKQN  
Sbjct 83 GSASHTVSGLVSL LAPGAKQN 103

> gi|33336661|gb|AAQ12998.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG LFAPGAKQN  
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|13448354|gb|AAK27000.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 34.7 bits (78), Expect = 1.2, Method: Composition-based stats.  
Identities = 14/21 (66%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AARTT+ FV +F+PGA+QN  
Sbjct 214 GGAARTTNSFVGMFSPGARQN 234

> gi|84380361|gb|ABC58410.1| polyprotein [Hepatitis C virus]  
Length=181

Score = 34.7 bits (78), Expect = 1.2, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+AAR TSG VSLF PGAKQ+  
Sbjct 146 GTAARATSGLVSLFTPGAKQD 166

> gi|37957197|gb|AAP03928.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G A T SGFVSL APGAKQN  
Sbjct 83 GXAGHTVSGFVSL LAPGAKQN 103

> gi|5918965|gb|AAD56198.1| polyprotein [Hepatitis C virus]  
Length=3010

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AARTT G SLF+PGA QN  
Sbjct 390 GQAARTTQGLTSLFSPGASQN 410

> gi|90658415|gb|ABD97104.1| polyprotein [Hepatitis C virus]  
Length=3021

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+AAR SG VSLF PGAKQN  
Sbjct 390 GNAARGASGIVSLFTPGAKQN 410

> gi|13448290|gb|AAK26968.1| polyprotein [Hepatitis C virus]  
Length=327

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+ +RTTSGF L APGAKQN  
Sbjct 215 GAVSRTTSGFAGLLAPGAKQN 235

> gi|33336593|gb|AAQ12964.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG LFAPGAKQN  
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|33637190|gb|AAQ23751.1| polyprotein [Hepatitis C virus]  
Length=190

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA R+T+GF LF+PGAKQN  
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|13448352|gb|AAK26999.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.  
Identities = 14/21 (66%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AARTT+ FV +F+PGA+QN  
Sbjct 214 GGAARTTNSFVGMFSPGARQN 234

> gi|13448287|gb|AAK26967.1| polyprotein [Hepatitis C virus]  
Length=327

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
' G+ +RTTSGF L APGAKQN  
Sbjct 215 GAVSRTTSGFAGLLAPGAKQN 235

> gi|33336539|gb|AAQ12937.1| polyprotein [Hepatitis C virus]  
gi|33336537|gb|AAQ12936.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG V L APGAKQN  
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|33337031|gb|AAQ13183.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.

Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SGF SLF P AKQN  
Sbjct 83 GSAGRTVSGFASLFTPDAKQN 103

> gi|33336801|gb|AAQ13068.1| polyprotein [Hepatitis C virus]  
gi|33336797|gb|AAQ13066.1| polyprotein [Hepatitis C virus]  
gi|33336793|gb|AAQ13064.1| polyprotein [Hepatitis C virus]  
gi|33336789|gb|AAQ13062.1| polyprotein [Hepatitis C virus]  
gi|33336787|gb|AAQ13061.1| polyprotein [Hepatitis C virus]  
gi|33336783|gb|AAQ13059.1| polyprotein [Hepatitis C virus]  
gi|33336759|gb|AAQ13047.1| polyprotein [Hepatitis C virus]  
gi|33336753|gb|AAQ13044.1| polyprotein [Hepatitis C virus]  
gi|33336745|gb|AAQ13040.1| polyprotein [Hepatitis C virus]  
gi|33336743|gb|AAQ13039.1| polyprotein [Hepatitis C virus]  
gi|33336741|gb|AAQ13038.1| polyprotein [Hepatitis C virus]  
gi|33336739|gb|AAQ13037.1| polyprotein [Hepatitis C virus]  
gi|33336541|gb|AAQ12938.1| polyprotein [Hepatitis C virus]  
gi|33336527|gb|AAQ12931.1| polyprotein [Hepatitis C virus]  
gi|33336523|gb|AAQ12929.1| polyprotein [Hepatitis C virus]  
gi|33336521|gb|AAQ12928.1| polyprotein [Hepatitis C virus]  
gi|33336519|gb|AAQ12927.1| polyprotein [Hepatitis C virus]  
gi|33336513|gb|AAQ12924.1| polyprotein [Hepatitis C virus]  
gi|33336503|gb|AAQ12919.1| polyprotein [Hepatitis C virus]  
gi|33336499|gb|AAQ12917.1| polyprotein [Hepatitis C virus]  
gi|33336497|gb|AAQ12916.1| polyprotein [Hepatitis C virus]  
gi|33336493|gb|AAQ12914.1| polyprotein [Hepatitis C virus]  
gi|33336491|gb|AAQ12913.1| polyprotein [Hepatitis C virus]  
gi|33336483|gb|AAQ12909.1| polyprotein [Hepatitis C virus]

Length=115

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG V L APGAKQN  
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|7649251|gb|AAF65815.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|37957131|gb|AAP03895.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTT+ FV +F+PGA+QN

Sbjct 83 GSAARTTNSFVGMFSPGARQN 103

> gi|56342211|dbj|BAD73983.1| polyprotein [Hepatitis C virus type 1b]  
Length=3010

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+AARTT GF SLF PG QN  
Sbjct 390 GAAARTTHGFTSLFTPGPSQN 410

> gi|33336659|gb|AAQ12997.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG LFAPGAKQN  
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|7649249|gb|AAF65814.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|33336725|gb|AAQ13030.1| polyprotein [Hepatitis C virus]

gi|33336713|gb|AAQ13024.1| polyprotein [Hepatitis C virus]  
gi|33336705|gb|AAQ13020.1| polyprotein [Hepatitis C virus]  
gi|33336699|gb|AAQ13017.1| polyprotein [Hepatitis C virus]  
gi|33336697|gb|AAQ13016.1| polyprotein [Hepatitis C virus]  
gi|33336683|gb|AAQ13009.1| polyprotein [Hepatitis C virus]  
gi|33336673|gb|AAQ13004.1| polyprotein [Hepatitis C virus]  
gi|33336671|gb|AAQ13003.1| polyprotein [Hepatitis C virus]  
gi|33336669|gb|AAQ13002.1| polyprotein [Hepatitis C virus]  
gi|33336667|gb|AAQ13001.1| polyprotein [Hepatitis C virus]  
gi|33336665|gb|AAQ13000.1| polyprotein [Hepatitis C virus]  
gi|33336657|gb|AAQ12996.1| polyprotein [Hepatitis C virus]  
gi|33336655|gb|AAQ12995.1| polyprotein [Hepatitis C virus]  
gi|33336653|gb|AAQ12994.1| polyprotein [Hepatitis C virus]  
gi|33336651|gb|AAQ12993.1| polyprotein [Hepatitis C virus]  
gi|33336649|gb|AAQ12992.1| polyprotein [Hepatitis C virus]  
gi|33336647|gb|AAQ12991.1| polyprotein [Hepatitis C virus]  
gi|33336643|gb|AAQ12989.1| polyprotein [Hepatitis C virus]  
gi|33336641|gb|AAQ12988.1| polyprotein [Hepatitis C virus]  
gi|33336637|gb|AAQ12986.1| polyprotein [Hepatitis C virus]  
gi|33336635|gb|AAQ12985.1| polyprotein [Hepatitis C virus]  
gi|33336633|gb|AAQ12984.1| polyprotein [Hepatitis C virus]  
gi|33336631|gb|AAQ12983.1| polyprotein [Hepatitis C virus]  
gi|33336629|gb|AAQ12982.1| polyprotein [Hepatitis C virus]

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gi|33336627|gb|AAQ12981.1| polyprotein [Hepatitis C virus]
gi|33336625|gb|AAQ12980.1| polyprotein [Hepatitis C virus]
gi|33336623|gb|AAQ12979.1| polyprotein [Hepatitis C virus]
gi|33336621|gb|AAQ12978.1| polyprotein [Hepatitis C virus]
gi|33336617|gb|AAQ12976.1| polyprotein [Hepatitis C virus]
gi|33336615|gb|AAQ12975.1| polyprotein [Hepatitis C virus]
gi|33336613|gb|AAQ12974.1| polyprotein [Hepatitis C virus]
gi|33336591|gb|AAQ12963.1| polyprotein [Hepatitis C virus]
gi|33336587|gb|AAQ12961.1| polyprotein [Hepatitis C virus]
gi|33336579|gb|AAQ12957.1| polyprotein [Hepatitis C virus]
gi|33336575|gb|AAQ12955.1| polyprotein [Hepatitis C virus]
gi|33336571|gb|AAQ12953.1| polyprotein [Hepatitis C virus]
gi|33336569|gb|AAQ12952.1| polyprotein [Hepatitis C virus]
gi|33336567|gb|AAQ12951.1| polyprotein [Hepatitis C virus]
gi|33336559|gb|AAQ12947.1| polyprotein [Hepatitis C virus]
gi|33336557|gb|AAQ12946.1| polyprotein [Hepatitis C virus]
gi|33336547|gb|AAQ12941.1| polyprotein [Hepatitis C virus]
gi|33336545|gb|AAQ12940.1| polyprotein [Hepatitis C virus]

```

Length=115

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

```

Query 1 GSAARTTSGFVSLFAPGAKQN 21
        GSA RT SG LFAPGAKQN
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

```

```

> gi|33336535|gb|AAQ12935.1| polyprotein [Hepatitis C virus]
gi|33336517|gb|AAQ12926.1| polyprotein [Hepatitis C virus]
gi|33336505|gb|AAQ12920.1| polyprotein [Hepatitis C virus]

```

Length=115

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

```

Query 1 GSAARTTSGFVSLFAPGAKQN 21
        GSA RT SG V L APGAKQN
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

```

```

> gi|13448283|gb|AAK26965.1| polyprotein [Hepatitis C virus]
Length=327

```

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

```

Query 1 GSAARTTSGFVSLFAPGAKQN 21
        G+ +RTTSGF L APGAKQN
Sbjct 215 GAVSRTTSGFAGLLAPGAKQN 235

```

```

> gi|33336973|gb|AAQ13154.1| polyprotein [Hepatitis C virus]
Length=115

```

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

```

Query 1 GSAARTTSGFVSLFAPGAKQN 21
        GSA RT SG SLF PGAKQN

```

Sbjct 83 GSAGRTVSGLASLFTPGAKQN 103

> gi|58220848|gb|AAW68051.1| envelope protein [synthetic construct]  
Length=578

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA +TSG SLF+PG KQN  
Sbjct 221 GSAAYSTSGLASLFSFGPKQN 241

> gi|33336543|gb|AAQ12939.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG V L APGAKQN  
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|62554071|dbj|BAD95611.1| polyprotein [Hepatitis C virus]  
Length=543

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA TTS F SLF+PG +QN  
Sbjct 200 GSAAHTTSRFTSLFSPGPQQN 220

> gi|33637198|gb|AAQ23755.1| polyprotein [Hepatitis C virus]  
Length=189

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA R+T+GF LF+PGAKQN  
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|33336877|gb|AAQ13106.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SL APGAKQN  
Sbjct 83 GSAGRTVSGLASLLAPGAKQN 103

> gi|33336983|gb|AAQ13159.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLF PGAKQN  
Sbjct 83 GSAGRTVSGLASLFTPGAKQN 103

> gi|13448646|gb|AAK27144.1| polyprotein [Hepatitis C virus]  
Length=315

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+TTSG SLF PGAKQ+  
Sbjct 210 GSAAQTTSGLASLFNPGAKQD 230

> gi|13344957|gb|AAK19132.1| polyprotein precursor [Hepatitis C virus]  
Length=415

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLFAPGA+QN  
Sbjct 390 GSAGRTVSGLASLFAPGARQN 410

> gi|7670915|gb|AAF66277.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTS V LF PGA+QN  
Sbjct 73 GSAARTTSSLVGLFNPGAQQN 93

> gi|33336663|gb|AAQ12999.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG LFAPGAKQN  
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|33336929|gb|AAQ13132.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21

GSA R SG SLFAPGAKQN  
 Sbjct 83 GSAGRAVSGLASLFAPGAKQN 103

> gi|33637206|gb|AAQ23759.1| polyprotein [Hepatitis C virus]  
 Length=189

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.  
 Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSA R+T+GF LF+PGAKQN  
 Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|7670913|gb|AAF66276.1| polyprotein precursor [Hepatitis C virus]  
 Length=186

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAARTTS V LF PGA+QN  
 Sbjct 73 GSAARTTSSLVGLFNPGAQQN 93

> gi|7650256|gb|AAF65959.1| polyprotein [Hepatitis C virus]  
 Length=3010

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.  
 Identities = 15/20 (75%), Positives = 16/20 (80%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20  
 G+ ARTTSGF SLF PGA Q  
 Sbjct 390 GATARTTSGFTSLFTPGASQ 409

> gi|84380358|gb|ABC58409.1| polyprotein [Hepatitis C virus]  
gi|84380351|gb|ABC58406.1| polyprotein [Hepatitis C virus]  
 Length=181

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.  
 Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 G+AAR TSG VSLF PGAKQ+  
 Sbjct 146 GTAARATSGLVSLFTPGAKQD 166

> gi|59474|emb|CAA37292.1| unnamed protein product [Hepatitis C virus]  
 Length=309

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
 Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 GSAAR+T+G SLF PGA+QN  
 Sbjct 262 GSAARSTAGVASLFTPGARQN 282

> gi|4927628|gb|AAD33205.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|4927605|gb|AAD33182.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|4927572|gb|AAD33149.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|33637212|gb|AAQ23762.1| polyprotein [Hepatitis C virus]  
Length=190

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA R+T+GF LF+PGAKQN  
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|33336529|gb|AAQ12932.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG V L APGAKQN  
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|16518682|gb|AAL24942.1| glycoprotein [Hepatitis C virus]  
gi|16518680|gb|AAL24941.1| glycoprotein [Hepatitis C virus]  
gi|16518678|gb|AAL24940.1| glycoprotein [Hepatitis C virus]  
gi|16518676|gb|AAL24939.1| glycoprotein [Hepatitis C virus]  
Length=85

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAAR T+G VSLF+PGAKQN  
Sbjct 55 GSAARATTGLVSLFSPGAKQN 75

> gi|20340011|gb|AAM19658.1| E1/E2 protein [Hepatitis C virus]  
Length=154

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+A+RTT+GF SLF PGA+QN  
Sbjct 105 GTASRTTAGFASLFNPGARQN 125

> gi|4469527|gb|AAD21301.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAAR TSG +LF+PGAKQ+  
Sbjct 214 GSAARATSGLANLFSPGAKQD 234

> gi|33336945|gb|AAQ13140.1| polyprotein [Hepatitis C virus]  
Length=115



Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLF PGAKQN  
Sbjct 83 GSAGRTVSGLASLFTPGAKQN 103

> gi|13448234|gb|AAK26941.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+TT+G VSL +PG KQN  
Sbjct 214 GSAAKTTAGLVSLLSPPGPKQN 234

> gi|22129793|ref|NP\_671491.1|  polyprotein [Hepatitis C virus]  
gi|2316098|gb|AAB66324.1|  polyprotein [Hepatitis C virus]  
Length=3011

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RTT+G V L PGAKQN  
Sbjct 390 GSAGRTTAGLVGLLTPGAKQN 410

> gi|4927597|gb|AAD33174.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 33.9 bits (76), Expect = 1.5, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|33336781|gb|AAQ13058.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG V L APGAKQN  
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|33336511|gb|AAQ12923.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG V L APGAKQN  
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|33336481|gb|AAQ12908.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG V L APGAKQN  
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|7670929|gb|AAF66284.1| polyprotein precursor [Hepatitis C virus]  
Length=186

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAARTTSG V LF PGA+ N  
Sbjct 73 GSAARTTSGLVGLFNPGAQHN 93

> gi|13448266|gb|AAK26957.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+TT+G VSL +PG KQN  
Sbjct 214 GSAAKTTAGLVSLSPGPKQN 234

> gi|33336755|gb|AAQ13045.1| polyprotein [Hepatitis C virus]  
gi|33336533|gb|AAQ12934.1| polyprotein [Hepatitis C virus]  
gi|33336487|gb|AAQ12911.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA T SG VSL APGAKQN  
Sbjct 83 GSAGHTVSGLVSLAPGAKQN 103

> gi|23955759|gb|AAN40611.1| polyprotein [Hepatitis C virus]  
Length=191

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GS ARTTSGF LF PGA QN  
Sbjct 73 GSVARTTSGFTGLFNPGASQN 93

> gi|13344961|gb|AAK19134.1| polyprotein precursor [Hepatitis C virus]  
Length=415

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG SLF PGAKQN  
Sbjct 390 GSAGRTVSGLASLFTPGAKQN 410

> gi|4469528|gb|AAD21302.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAAR TSG +LF+PGAKQ+  
Sbjct 214 GSAARATSGLANLFSPGAKQD 234

> gi|13448232|gb|AAK26940.1| polyprotein [Hepatitis C virus]  
gi|13448230|gb|AAK26939.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+TT+G VSL +PG KQN  
Sbjct 214 GSAAKTTAGLVSLSPGPKQN 234

> gi|13448226|gb|AAK26937.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA+TT+G VSL +PG KQN  
Sbjct 214 GSAAKTTAGLVSLSPGPKQN 234

> gi|4927608|gb|AAD33185.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|4927622|gb|AAD33199.1| polyprotein [Hepatitis C virus]  
gi|4927598|gb|AAD33175.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|4927568|gb|AAD33145.1| polyprotein [Hepatitis C virus]  
Length=175

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAART +G SLF+PGAKQN  
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|20340013|gb|AAM19659.1| E1/E2 protein [Hepatitis C virus]  
Length=154

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G+A+RTT+GF SLF PGA+QN  
Sbjct 105 GTASRTTAGFASLFNPGARQN 125

> gi|221512|dbj|BAA00705.1| structural protein [Hepatitis C virus]  
Length=513

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AAR SG VSLF PGAKQN  
Sbjct 390 GQAARAMSGLVSLFTPGAKQN 410

> gi|33336795|gb|AAQ13065.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG V L APGAKQN  
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|33336763|gb|AAQ13049.1| polyprotein [Hepatitis C virus]  
Length=115

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSA RT SG V L APGAKQN  
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|13448454|gb|AAK27049.1| polyprotein [Hepatitis C virus]  
Length=326

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
GSAA T+GF LF PGAKQN  
Sbjct 214 GSAAHATAGFAGLFTPGAKQN 234

> gi|53801722|gb|AAU94034.1| polyprotein [Hepatitis C virus]  
Length=426

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
Identities = 14/21 (66%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
G AAR+TSGF+ LF PG+KQ+  
Sbjct 199 GVAARSTSGFIGLFQPGSKQD 219

> gi|6521009|dbj|BAA88057.1| polyprotein [Hepatitis C virus (isolate VAT96)]  
gi|82007035|sp|Q9QAX1|POLG\_HCVVA Genome polyprotein [Contains: Core protein p21 (Caps C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]  
 Length=3033

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.  
 Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21  
 G AARTT G VSLF PG++QN  
 Sbjct 390 GHAAARTTHGLVSLFTPGSQQN 410

Get selected sequences

Select all

Deselect all

Distance tree of results

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Jul 21, 2006 3:13 AM

Number of letters in database: 1,312,719,415

Number of sequences in database: 3,807,609

Lambda K H  
 0.311 0.123 0.341

Gapped

Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 3807609

Number of Hits to DB: 4479366

Number of extensions: 36593

Number of successful extensions: 28

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 28

Number of HSP's successfully gapped: 0

Length of query: 21

Length of database: 1312719415

Length adjustment: 0

Effective length of query: 21

Effective length of database: 1312719415

Effective search space: 27567107715

Effective search space used: 27567107715

T: 11

A: 40

X1: 16 (7.2 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 42 (20.8 bits)

S2: 70 (31.6 bits)



# results of BLAST

BLASTP 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153602248-17953-92119523316.BLASTQ4

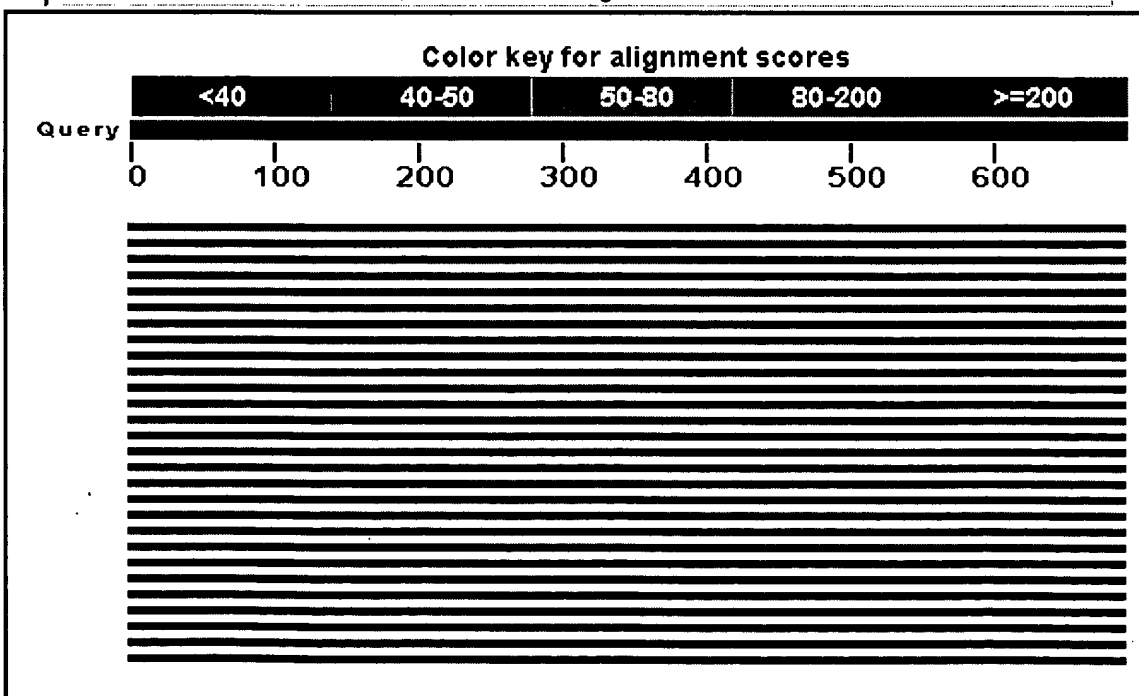
**Database:** Non-redundant SwissProt sequences  
208,958 sequences; 78,544,511 total letters

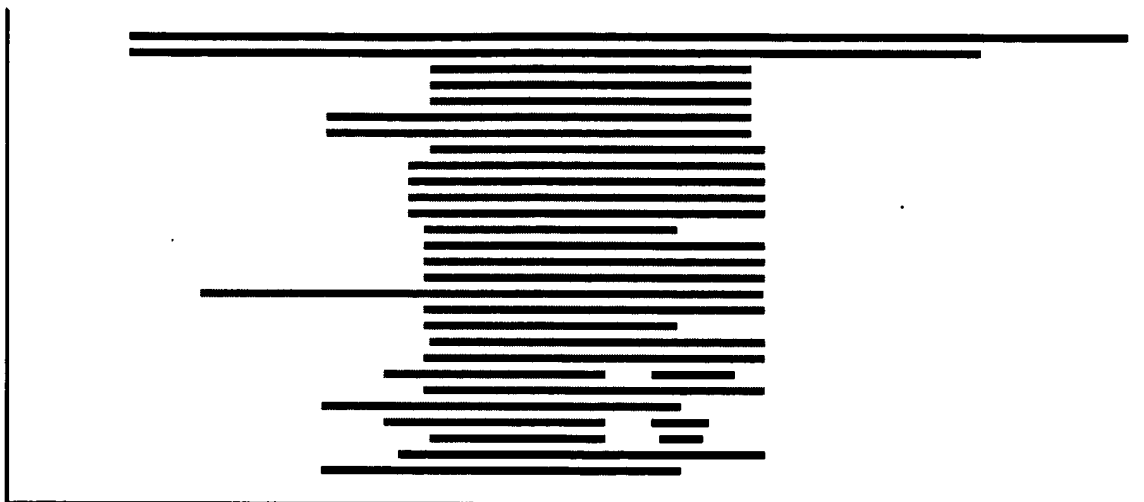
If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)  
[Taxonomy reports](#)

**Query=**  
Length=685

## Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



Distance tree of results **NEW**

Sequences producing significant alignments:			Score (Bits)	E Value
<a href="#">gi 130455 sp P26664 POLG_HCV1</a>	Genome polyprotein [Contains: C...		1302	0.0
<a href="#">gi 130461 sp P27958 POLG_HCVH</a>	Genome polyprotein [Contains: C...		1268	0.0
<a href="#">gi 130458 sp P26663 POLG_HCVBK</a>	Genome polyprotein [Contains: ...		1232	0.0
<a href="#">gi 266820 sp Q00269 POLG_HCVJT</a>	Genome polyprotein [Contains: ...		1229	0.0
<a href="#">gi 81992806 sp Q81754 POLG_HCVH9</a>	Genome polyprotein [Contains...		1229	0.0
<a href="#">gi 68565847 sp Q9WMX2 POLG_HCVCO</a>	Genome polyprotein [Contains...		1228	0.0
<a href="#">gi 266821 sp P29846 POLG_HCVTW</a>	Genome polyprotein [Contains: ...		1226	0.0
<a href="#">gi 130469 sp P26662 POLG_HCVJA</a>	Genome polyprotein [Contains: ...		1221	0.0
<a href="#">gi 81960062 sp Q913D4 POLG_HCVIN</a>	Genome polyprotein [Contains...		1207	0.0
<a href="#">gi 81924266 sp O91936 POLG_HCVSA</a>	Genome polyprotein [Contains...		1150	0.0
<a href="#">gi 81924482 sp O92529 POLG_HCVT5</a>	Genome polyprotein [Contains...		1146	0.0
<a href="#">gi 81985682 sp Q5I2N3 POLG_HCV6A</a>	Genome polyprotein [Contains...		1142	0.0
<a href="#">gi 81924483 sp O92530 POLG_HCVVN</a>	Genome polyprotein [Contains...		1134	0.0
<a href="#">gi 81924484 sp O92531 POLG_HCVVO</a>	Genome polyprotein [Contains...		1133	0.0
<a href="#">gi 81921386 sp O39929 POLG_HCVED</a>	Genome polyprotein [Contains...		1130	0.0
<a href="#">gi 81921385 sp O39928 POLG_HCVEV</a>	Genome polyprotein [Contains...		1127	0.0
<a href="#">gi 81921384 sp O39927 POLG_HCVEU</a>	Genome polyprotein [Contains...		1122	0.0
<a href="#">gi 81924485 sp O92532 POLG_HCVVP</a>	Genome polyprotein [Contains...		1121	0.0
<a href="#">gi 81938291 sp Q68798 POLG_HCVJL</a>	Genome polyprotein [Contains...		1121	0.0
<a href="#">gi 81992783 sp Q81258 POLG_HCVNZ</a>	Genome polyprotein [Contains...		1084	0.0
<a href="#">gi 75566979 sp Q81495 POLG_HCVK3</a>	Genome polyprotein [Contains...		1079	0.0
<a href="#">gi 82007035 sp Q9QAX1 POLG_HCVVA</a>	Genome polyprotein [Contains...		1079	0.0
<a href="#">gi 82004405 sp Q9DHD6 POLG_HCVJP</a>	Genome polyprotein [Contains...		1073	0.0
<a href="#">gi 130468 sp P26661 POLG_HCVJ8</a>	Genome polyprotein [Contains: ...		1070	0.0
<a href="#">gi 81992797 sp Q81487 POLG_HCVTR</a>	Genome polyprotein [Contains...		1065	0.0
<a href="#">gi 130466 sp P26660 POLG_HCVJ6</a>	Genome polyprotein [Contains: ...		1065	0.0
<a href="#">gi 81938267 sp Q68749 POLG_HCVBB</a>	Genome polyprotein [Contains...		1064	0.0
<a href="#">gi 81938293 sp Q68801 POLG_HCVJK</a>	Genome polyprotein [Contains...		1063	0.0
<a href="#">gi 81967359 sp Q99IB8 POLG_HCVJF</a>	Genome polyprotein [Contains...		1043	0.0
<a href="#">gi 68565638 sp Q69422 POLG_GBVV</a>	Genome polyprotein [Contains...		400	1e-110
<a href="#">gi 46396995 sp Q96662 POLG_BVDVC</a>	Genome polyprotein [Contains...		81.3	1e-14
<a href="#">gi 1346739 sp P19711 POLG_BVDVN</a>	Genome polyprotein [Contains...		79.7	3e-14
<a href="#">gi 400808 sp Q01499 POLG_BVDVS</a>	Genome polyprotein [Contains: ...		79.0	5e-14
<a href="#">gi 130457 sp P21530 POLG_CSFVB</a>	Genome polyprotein [Contains: ...		75.5	5e-13
<a href="#">gi 14917023 sp P19712 POLG_CSFVA</a>	Genome polyprotein [Contains...		75.5	6e-13
<a href="#">gi 130522 sp P04517 POLG_TEV</a>	Genome polyprotein [Contains: Pl...		65.1	8e-10
<a href="#">gi 3914417 sp Q84934 POLG_PPVSK</a>	Genome polyprotein [Contains...		56.6	3e-07



gi 130505 sp P17766 POLG_PPVNA	Genome polyprotein [Contains: ...	56.2	4e-07	
gi 464430 sp P17767 POLG_PPVRA	Genome polyprotein [Contains: ...	55.5	6e-07	
gi 6226884 sp P13529 POLG_PPVD	Genome polyprotein [Contains: ...	55.5	6e-07	
gi 21431801 sp P31999 POLG_LMV0	Genome polyprotein [Contains:...	55.1	7e-07	
gi 3914412 sp P89509 POLG_TUMVJ	Genome polyprotein [Contains:...	55.1	8e-07	
gi 417510 sp Q01500 POLG_PEMVC	Genome polyprotein [Contains: ...	55.1	9e-07	
gi 548557 sp Q02597 POLG_TUMVQ	Genome polyprotein [Contains: ...	54.7	1e-06	
gi 56757564 sp P05769 POLG_MVEV5	Genome polyprotein [Contains...	53.9	2e-06	
gi 21431806 sp P21231 POLG_SBMVN	Genome polyprotein [Contains...	53.5	3e-06	
gi 3914399 sp P89876 POLG_LMVE	Genome polyprotein [Contains: ...	52.0	8e-06	
gi 62900634 sp Q6XW15 POLG_BTMV	Genome polyprotein [Contains:...	51.6	9e-06	G
gi 3914397 sp Q65399 POLG_BCMVN	Genome polyprotein [Contains:...	51.6	9e-06	
gi 3914418 sp Q89330 POLG_ZYMVR	Genome polyprotein [Contains:...	51.2	1e-05	
gi 3914419 sp Q90069 POLG_SBMVG	Genome polyprotein [Contains:...	50.4	2e-05	
gi 266813 sp P29990 POLG_DEN26	Genome polyprotein [Contains: ...	50.4	2e-05	
gi 3915808 sp P18479 POLG_ZYMVC	Genome polyprotein [Contains:...	50.1	2e-05	
gi 20141657 sp O36979 POLG_ZYMVS	Genome polyprotein [Contains...	49.7	4e-05	
gi 68067450 sp P17765 POLG_BYMV	Genome polyprotein [Contains:...	49.7	4e-05	
gi 1709704 sp P14340 POLG_DEN2N	Genome polyprotein [Contains:...	49.3	5e-05	
gi 130490 sp P27395 POLG_JAEV1	Genome polyprotein [Contains: ...	49.3	5e-05	
gi 417507 sp P32886 POLG_JAEVJ	Genome polyprotein [Contains: ...	49.3	5e-05	
gi 266814 sp P29991 POLG_DEN27	Genome polyprotein [Contains: ...	48.9	6e-05	
gi 130491 sp P19110 POLG_JAEV5	Genome polyprotein [Contains: ...	48.9	7e-05	
gi 130428 sp P07564 POLG_DEN2J	Genome polyprotein [Contains: ...	48.5	9e-05	
gi 46396621 sp Q85197 POLG_PVMA	Genome polyprotein [Contains:...	48.1	1e-04	
gi 464429 sp P33515 POLG_MCFA	Genome polyprotein [Contains: C...	48.1	1e-04	G
gi 39932633 sp  P27914_2	[Segment 2 of 2] Genome polyprotein ...	47.8	1e-04	
gi 130430 sp P12823 POLG_DEN2P	Genome polyprotein [Contains: ...	47.8	1e-04	
gi 130509 sp P29152 POLG_PSBMV	Genome polyprotein [Contains: ...	47.4	2e-04	
gi 400818 sp Q02963 POLG_PVYHU	Genome polyprotein [Contains: ...	46.2	4e-04	
gi 8247947 sp P09814 POLG_TVMV	Genome polyprotein [Contains: ...	46.2	4e-04	G
gi 3914379 sp Q65730 POLG_BSTV1	Genome polyprotein [Contains:...	45.8	4e-04	
gi 41019473 sp P09866 POLG_DEN4	Genome polyprotein [Contains:...	45.4	6e-04	
gi 130437 sp P27915 POLG_DEN3	Genome polyprotein [Contains: C...	45.4	6e-04	
gi 1346743 sp P18247 POLG_PVYN	Genome polyprotein [Contains: ...	45.1	9e-04	
gi 130530 sp P19901 POLG_YEFV2	Genome polyprotein [Contains: ...	44.7	0.001	
gi 130529 sp P03314 POLG_YEFV1	Genome polyprotein [Contains: ...	44.7	0.001	
gi 26006959 sp O60231 DHX16_HUMAN	Putative pre-mRNA-splicing ...	43.1	0.003	G
gi 38502930 sp Q7YR39 DHX16_PANTR	Putative pre-mRNA-splicing ...	43.1	0.003	G
gi 37999909 sp P06935 POLG_WNV	Genome polyprotein [Contains: ...	43.1	0.004	G
gi 19862987 sp Q10752 CDC28_SCHPO	Putative ATP-dependent RNA hel	42.0	0.007	
gi 464427 sp P33478 POLG_DEN1S	Genome polyprotein [Contains: ...	41.6	0.010	
gi 6093763 sp O56075 POLG_PEMVM	Genome polyprotein [Contains:...	40.4	0.023	
gi 46396755 sp P90245 POL1_BAMMN	Genome polyprotein 1 [Contai...	39.7	0.032	
gi 1709707 sp Q01299 POLG_TBEVH	Genome polyprotein [Contains:...	39.7	0.035	
gi 6226885 sp P14336 POLG_TBEVW	Genome polyprotein [Contains:...	39.3	0.042	
gi 1709706 sp Q01901 POLG_PRSVH	Genome polyprotein [Contains:...	39.3	0.047	
gi 549698 sp P36009 DHR2_YEAST	Probable ATP-dependent RNA hel...	39.3	0.050	G
gi 464428 sp P29837 POLG_LANVT	Genome polyprotein [Contains: ...	38.9	0.053	
gi 54041622 sp P15043 RECQ_ECOLI	ATP-dependent DNA helicase recQ	38.1	0.11	
gi 22654276 sp O94762 RECQ5_HUMAN	ATP-dependent DNA helicase Q5	37.7	0.13	G
gi 19859341 sp P40724 RECQ_SALTY	ATP-dependent DNA helicase recQ	37.7	0.14	
gi 17366114 sp Q9VGI8 BLM_DROME	Bloom syndrome protein homolo...	37.4	0.16	G
gi 130494 sp P14335 POLG_KUNJM	Genome polyprotein [Contains: ...	37.4	0.19	
gi 20137928 sp Q9BKQ8 DHX35_CAEEL	Probable ATP-dependent RNA hel	37.0	0.21	G
gi 130520 sp P07720 POLG_TBEVS	Genome polyprotein [Contains: ...	37.0	0.22	
gi 20137971 sp Q9H5Z1 DHX35_HUMAN	Probable ATP-dependent RNA hel	36.6	0.30	G
gi 21431859 sp P34305 RHA2_CAEEL	Putative ATP-dependent RNA heli	36.6	0.30	G

<a href="#">gi 61212955 sp Q5RBD4 DHX35_PONPY</a>	Probable ATP-dependent RNA hel	<a href="#">36.2</a>	0.36	
<a href="#">gi 464912 sp P35187 SGS1_YEAST</a>	ATP-dependent helicase SGS1 (Heli	<a href="#">35.0</a>	0.88	<b>G</b>
<a href="#">gi 18202817 sp Q9CL21 RECQ_PASMU</a>	ATP-dependent DNA helicase recQ	<a href="#">35.0</a>	0.98	
<a href="#">gi 2500112 sp P71359 RECQ_HAEIN</a>	ATP-dependent DNA helicase recQ	<a href="#">35.0</a>	0.98	
<a href="#">gi 1705486 sp P54132 BLM_HUMAN</a>	Bloom syndrome protein (RecQ p...	<a href="#">33.1</a>	3.3	<b>G</b>
<a href="#">gi 5921178 sp O88700 BLM_MOUSE</a>	Bloom syndrome protein homolog (m	<a href="#">33.1</a>	3.5	<b>G</b>
<a href="#">gi 130804 sp P20095 PRP2_YEAST</a>	Pre-mRNA-splicing factor ATP-depe	<a href="#">33.1</a>	3.6	<b>G</b>
<a href="#">gi 3915519 sp O45244 DHX16_CAEEL</a>	Probable pre-mRNA-splicing f...	<a href="#">33.1</a>	3.6	<b>G</b>
<a href="#">gi 24212040 sp Q8UDM3 MURE_AGR5</a>	UDP-N-acetylmuramoylalanyl-D...	<a href="#">32.7</a>	4.3	<b>G</b>
<a href="#">gi 17366086 sp Q9I920 BLM_CHICK</a>	Bloom syndrome protein homolog	<a href="#">32.0</a>	6.5	<b>G</b>
<a href="#">gi 730353 sp Q04538 POLG_POWVL</a>	Genome polyprotein [Contains: ...	<a href="#">32.0</a>	7.0	
<a href="#">gi 59803058 sp Q9SEL7 DEGP5_ARATH</a>	Protease Do-like 5, chloroplas	<a href="#">31.6</a>	8.9	<b>G</b>

## Alignments

Get selected sequences

Select all

Deselect all

Distance tree of results

> [gi|130455|sp|P26664|POLG\\_HCV1](#) Genome polyprotein [Contains: Core protein p21 (Caps: C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]  
Length=3011

Score = 1302 bits (3370), Expect = 0.0, Method: Composition-based stats.  
Identities = 683/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKGSSGGPLLCAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	1147	DSRGSLLSPRPISYLKGSSGGPLLCAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVF TDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVF TDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	
Sbjct	1207	SPVF TDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLV ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKLV ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLV ALGINAVAYYRGLDVSVIP TSGDVVVVVATDALMTGYTG	1446



# results of BLAST

BLASTP 2.2.14 [May-07-2006]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

**Reference:**

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153602163-31376-31136956327.BLASTQ1

Database: pat

301,733 sequences; 55,455,050 total letters

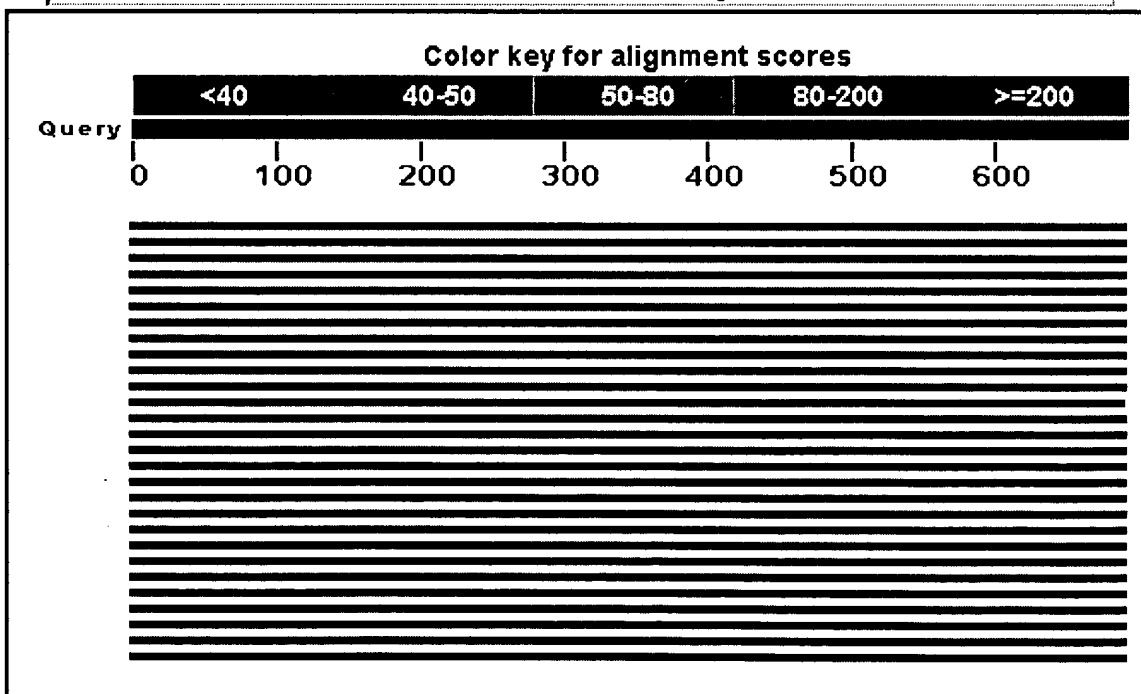
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)  
[Taxonomy reports](#)

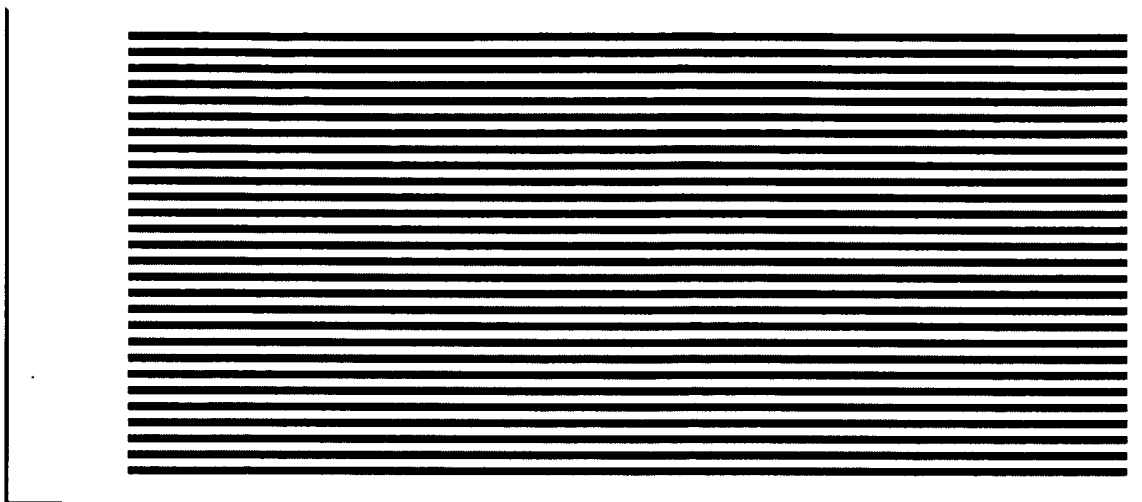
Query=

Length=685

## Distribution of 102 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments



Distance tree of results NEW

Sequences producing significant alignments:			Score (Bits)	E Value
<a href="#">gi 594200 gb AAA55807.1 </a>	Sequence 53 from Patent EP 0318216 >...		<a href="#">1303</a>	0.0
<a href="#">gi 31689077 gb AAP61048.1 </a>	Sequence 2 from patent US 6538123 ...		<a href="#">1302</a>	0.0
<a href="#">gi 21508650 gb AAM58139.1 </a>	Sequence 1 from patent US 6379886		<a href="#">1302</a>	0.0
<a href="#">gi 593530 gb AAA55137.1 </a>	Sequence 2 from Patent EP 0388232		<a href="#">1302</a>	0.0
<a href="#">gi 14101397 gb AAE53714.1 </a>	Sequence 66 from patent US 6150087		<a href="#">1301</a>	0.0
<a href="#">gi 14101433 gb AAE53750.1 </a>	Sequence 138 from patent US 6150087		<a href="#">1299</a>	0.0
<a href="#">gi 594199 gb AAA55806.1 </a>	Sequence 47 from Patent EP 0318216 >...		<a href="#">1299</a>	0.0
<a href="#">gi 14101409 gb AAE53726.1 </a>	Sequence 89 from patent US 6150087		<a href="#">1298</a>	0.0
<a href="#">gi 592432 gb AAA54039.1 </a>	Sequence 14 from Patent WO 8904669		<a href="#">1297</a>	0.0
<a href="#">gi 14101402 gb AAE53719.1 </a>	Sequence 75 from patent US 6150087		<a href="#">1297</a>	0.0
<a href="#">gi 33737406 gb AAQ41059.1 </a>	Sequence 23 from patent US 6576417...		<a href="#">1293</a>	0.0
<a href="#">gi 14101391 gb AAE53708.1 </a>	Sequence 54 from patent US 6150087		<a href="#">1292</a>	0.0
<a href="#">gi 14101424 gb AAE53741.1 </a>	Sequence 124 from patent US 6150087		<a href="#">1290</a>	0.0
<a href="#">gi 91165235 gb ABE25678.1 </a>	Sequence 3 from patent US 7022323		<a href="#">1286</a>	0.0
<a href="#">gi 12828946 gb AAE50646.1 </a>	Sequence 2 from patent US 6127116		<a href="#">1286</a>	0.0
<a href="#">gi 6001418 gb AAE22380.1 </a>	Sequence 2 from patent US 5854001 >...		<a href="#">1285</a>	0.0
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<a href="#">gi 14124296 gb AAE60492.1 </a>	Sequence 6 from patent US 6194140 ...		<a href="#">1285</a>	0.0
<a href="#">gi 6001417 gb AAE22379.1 </a>	Sequence 1 from patent US 5854001 >...		<a href="#">1284</a>	0.0
<a href="#">gi 75915319 gb ABA29873.1 </a>	Sequence 20 from patent US 6921634...		<a href="#">1283</a>	0.0
<a href="#">gi 14103322 gb AAE54756.1 </a>	Sequence 5 from patent US 6153421		<a href="#">1283</a>	0.0
<a href="#">gi 12828947 gb AAE50647.1 </a>	Sequence 20 from patent US 6127116		<a href="#">1282</a>	0.0
<a href="#">gi 56627907 gb AAW06244.1 </a>	Sequence 2 from patent US 6797809 ...		<a href="#">1271</a>	0.0
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<a href="#">gi 91175831 gb ABE26525.1 </a>	Sequence 6 from patent US 7022830 ...		<a href="#">1246</a>	0.0
<a href="#">gi 91175834 gb ABE26528.1 </a>	Sequence 9 from patent US 7022830 ...		<a href="#">1245</a>	0.0
<a href="#">gi 91175832 gb ABE26526.1 </a>	Sequence 7 from patent US 7022830 ...		<a href="#">1244</a>	0.0

<a href="#">gi 56611440 gb AAW04090.1 </a>	Sequence 4 from patent US 6790612 ...	<a href="#">1235</a>	0.0
<a href="#">gi 56611452 gb AAW04102.1 </a>	Sequence 18 from patent US 6790612...	<a href="#">1234</a>	0.0
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<a href="#">gi 56611446 gb AAW04096.1 </a>	Sequence 11 from patent US 6790612...	<a href="#">1234</a>	0.0
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<a href="#">gi 91175836 gb ABE26530.1 </a>	Sequence 11 from patent US 7022830...	<a href="#">1232</a>	0.0
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<a href="#">gi 15110179 gb AAE67843.1 </a>	Sequence 36 from patent US 6217872...	<a href="#">1232</a>	0.0
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<a href="#">gi 33759553 gb AAQ52043.1 </a>	Sequence 4 from patent US 6593083 ...	<u>531</u>	1e-150
<a href="#">gi 40114189 gb AAR55316.1 </a>	Sequence 265 from patent US 661333...	<u>528</u>	9e-150
<a href="#">gi 33759592 gb AAQ52082.1 </a>	Sequence 59 from patent US 6593083...	<u>525</u>	1e-148
<a href="#">gi 40160940 gb AAR67292.1 </a>	Sequence 1 from patent US 6635257	<u>523</u>	3e-148
<a href="#">gi 17915386 gb AAE84112.1 </a>	Sequence 2 from patent US 6306579 ...	<u>520</u>	3e-147
<a href="#">gi 40114191 gb AAR55318.1 </a>	Sequence 267 from patent US 661333...	<u>518</u>	9e-147
<a href="#">gi 53920899 gb AAU97762.1 </a>	Sequence 36 from patent US 6727092...	<u>516</u>	5e-146
<a href="#">gi 53920898 gb AAU97761.1 </a>	Sequence 32 from patent US 6727092...	<u>516</u>	5e-146
<a href="#">gi 40114190 gb AAR55317.1 </a>	Sequence 266 from patent US 661333...	<u>516</u>	5e-146
<a href="#">gi 53920895 gb AAU97758.1 </a>	Sequence 20 from patent US 6727092...	<u>515</u>	7e-146
<a href="#">gi 53920897 gb AAU97760.1 </a>	Sequence 28 from patent US 6727092...	<u>515</u>	7e-146
<a href="#">gi 53920896 gb AAU97759.1 </a>	Sequence 25 from patent US 6727092...	<u>515</u>	7e-146
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<a href="#">gi 53920894 gb AAU97757.1 </a>	Sequence 18 from patent US 6727092...	<u>515</u>	9e-146
<a href="#">gi 53920901 gb AAU97764.1 </a>	Sequence 40 from patent US 6727092...	<u>514</u>	2e-145
<a href="#">gi 40114199 gb AAR55325.1 </a>	Sequence 274 from patent US 661333...	<u>513</u>	3e-145
<a href="#">gi 40114194 gb AAR55321.1 </a>	Sequence 270 from patent US 661333...	<u>511</u>	9e-145
<a href="#">gi 40160941 gb AAR67293.1 </a>	Sequence 2 from patent US 6635257	<u>511</u>	1e-144
<a href="#">gi 40114197 gb AAR55323.1 </a>	Sequence 272 from patent US 661333...	<u>510</u>	2e-144
<a href="#">gi 3211590 gb AAC21350.1 </a>	I83293 Sequence 84 from patent US 57...	<u>509</u>	3e-144
<a href="#">gi 42711673 gb AAS35883.1 </a>	Sequence 57 from patent US 6689368...	<u>509</u>	4e-144
<a href="#">gi 40114193 gb AAR55320.1 </a>	Sequence 269 from patent US 661333...	<u>509</u>	5e-144
<a href="#">gi 40114196 gb AAR55322.1 </a>	Sequence 271 from patent US 661333...	<u>509</u>	6e-144
<a href="#">gi 40114200 gb AAR55326.1 </a>	Sequence 275 from patent US 661333...	<u>508</u>	1e-143
<a href="#">gi 40114198 gb AAR55324.1 </a>	Sequence 273 from patent US 661333...	<u>508</u>	1e-143
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<a href="#">gi 40114201 gb AAR55327.1 </a>	Sequence 276 from patent US 661333...	<u>506</u>	4e-143
<a href="#">gi 40114192 gb AAR55319.1 </a>	Sequence 268 from patent US 661333...	<u>504</u>	1e-142
<a href="#">gi 40153769 gb AAR65055.1 </a>	Sequence 5 from patent US 6630298 ...	<u>488</u>	9e-138
<a href="#">gi 15108286 gb AAE67322.1 </a>	Sequence 45 from patent US 6210962...	<u>487</u>	2e-137
<a href="#">gi 15108277 gb AAE67313.1 </a>	Sequence 7 from patent US 6210962 ...	<u>484</u>	2e-136
<a href="#">gi 91126695 gb ABE13386.1 </a>	Sequence 85 from patent US 6977144	<u>479</u>	4e-135
<a href="#">gi 40114202 gb AAR55328.1 </a>	Sequence 277 from patent US 661333...	<u>459</u>	5e-129
<a href="#">gi 40114204 gb AAR55329.1 </a>	Sequence 278 from patent US 661333...	<u>457</u>	3e-128
<a href="#">gi 594197 gb AAA55804.1 </a>	Sequence 41 from Patent EP 0318216	<u>454</u>	3e-127

<a href="#">gi 14101374 gb AAE53691.1 </a>	Sequence 20 from patent US 6150087	<a href="#">451</a>	2e-126
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<a href="#">gi 3211582 gb AAC21342.1 I83285</a>	Sequence 68 from patent US 57...	<a href="#">392</a>	9e-109
<a href="#">gi 62786768 gb AAY06807.1 </a>	Sequence 2 from patent US 6870043	<a href="#">388</a>	2e-107
<a href="#">gi 5997134 gb AAE20681.1 </a>	Sequence 15 from patent US 5849532 ...	<a href="#">387</a>	3e-107
<a href="#">gi 5997168 gb AAE20715.1 </a>	Sequence 183 from patent US 5849532...	<a href="#">385</a>	7e-107
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<a href="#">gi 47268062 gb AAT26683.1 </a>	Sequence 401 from patent US 672016...	<a href="#">384</a>	2e-106
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<a href="#">gi 47267592 gb AAT26448.1 </a>	Sequence 83 from patent US 6720166...	<a href="#">361</a>	2e-99
<a href="#">gi 91126697 gb ABE13388.1 </a>	Sequence 87 from patent US 6977144	<a href="#">360</a>	5e-99
<a href="#">gi 47268052 gb AAT26678.1 </a>	Sequence 395 from patent US 672016...	<a href="#">357</a>	3e-98
<a href="#">gi 5991332 gb AAE18141.1 </a>	Sequence 10 from patent US 5843639 ...	<a href="#">344</a>	2e-94
<a href="#">gi 15108287 gb AAE67323.1 </a>	Sequence 46 from patent US 6210962...	<a href="#">339</a>	9e-93
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<a href="#">gi 56629275 gb AAW06836.1 </a>	Sequence 24 from patent US 6800456	<a href="#">323</a>	7e-88
<a href="#">gi 56629260 gb AAW06821.1 </a>	Sequence 1 from patent US 6800456	<a href="#">322</a>	9e-88
<a href="#">gi 56629261 gb AAW06822.1 </a>	Sequence 3 from patent US 6800456	<a href="#">321</a>	2e-87
<a href="#">gi 91126698 gb ABE13389.1 </a>	Sequence 88 from patent US 6977144	<a href="#">318</a>	2e-86
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<a href="#">gi 7224496 gb AAE24663.1 </a>	Sequence 43 from patent US 5910405	<a href="#">309</a>	1e-83
<a href="#">gi 14101373 gb AAE53690.1 </a>	Sequence 18 from patent US 6150087	<a href="#">308</a>	1e-83
<a href="#">gi 56629269 gb AAW06830.1 </a>	Sequence 12 from patent US 6800456	<a href="#">308</a>	1e-83
<a href="#">gi 56644596 gb AAW12758.1 </a>	Sequence 14 from patent US 6815159	<a href="#">307</a>	3e-83
<a href="#">gi 56644595 gb AAW12757.1 </a>	Sequence 13 from patent US 6815159	<a href="#">307</a>	3e-83
<a href="#">gi 56644600 gb AAW12762.1 </a>	Sequence 18 from patent US 6815159	<a href="#">306</a>	6e-83
<a href="#">gi 56644597 gb AAW12759.1 </a>	Sequence 15 from patent US 6815159	<a href="#">306</a>	6e-83
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<a href="#">gi 56644599 gb AAW12761.1 </a>	Sequence 17 from patent US 6815159	<a href="#">305</a>	2e-82
<a href="#">gi 56629271 gb AAW06832.1 </a>	Sequence 16 from patent US 6800456	<a href="#">303</a>	4e-82
<a href="#">gi 91126699 gb ABE13390.1 </a>	Sequence 89 from patent US 6977144	<a href="#">303</a>	5e-82
<a href="#">gi 14480058 gb AAE62020.1 </a>	Sequence 4 from patent US 6197536	<a href="#">300</a>	6e-81
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<a href="#">gi 40194407 gb AAR78448.1 </a>	Sequence 6 from patent US 6653127 ...	<u>295</u>	2e-79
<a href="#">gi 56629273 gb AAW06834.1 </a>	Sequence 20 from patent US 6800456	<u>294</u>	2e-79
<a href="#">gi 56629272 gb AAW06833.1 </a>	Sequence 18 from patent US 6800456	<u>294</u>	3e-79
<a href="#">gi 40194405 gb AAR78446.1 </a>	Sequence 4 from patent US 6653127 ...	<u>294</u>	3e-79
<a href="#">gi 40194409 gb AAR78450.1 </a>	Sequence 8 from patent US 6653127 ...	<u>293</u>	8e-79
<a href="#">gi 56629274 gb AAW06835.1 </a>	Sequence 22 from patent US 6800456	<u>291</u>	3e-78
<a href="#">gi 14480059 gb AAE62021.1 </a>	Sequence 5 from patent US 6197536	<u>289</u>	9e-78
<a href="#">gi 40148288 gb AAR63521.1 </a>	Sequence 11 from patent US 6623921...	<u>287</u>	3e-77
<a href="#">gi 14480057 gb AAE62019.1 </a>	Sequence 3 from patent US 6197536	<u>282</u>	1e-75
<a href="#">gi 91126700 gb ABE13391.1 </a>	Sequence 90 from patent US 6977144	<u>280</u>	7e-75
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<a href="#">gi 1248641 emb CAA01932.1 </a>	PT-NANBH polyprotein [synthetic const	<u>276</u>	7e-74
<a href="#">gi 14101398 gb AAE53715.1 </a>	Sequence 68 from patent US 6150087...	<u>276</u>	7e-74
<a href="#">gi 91126694 gb ABE13385.1 </a>	Sequence 84 from patent US 6977144	<u>274</u>	3e-73
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<a href="#">gi 3990922 gb AAC84349.1 AR000772</a>	Sequence 48 from patent US 573	<a href="#">60.8</a>	5e-09
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<a href="#">gi 3990925 gb AAC84352.1 AR000775</a>	Sequence 51 from patent US 573	<a href="#">52.4</a>	2e-06
<a href="#">gi 5957228 gb AAE07902.1 </a>	Sequence 3 from patent US 5800982	<a href="#">52.4</a>	2e-06
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<a href="#">gi 15554472 emb CAC69561.1 </a>	unnamed protein product [synthetic c	<a href="#">51.2</a>	5e-06
<a href="#">gi 15554470 emb CAC69560.1 </a>	unnamed protein product [synthetic c	<a href="#">51.2</a>	5e-06
<a href="#">gi 15554488 emb CAC69569.1 </a>	unnamed protein product [synthetic c	<a href="#">50.8</a>	6e-06
<a href="#">gi 15554468 emb CAC69559.1 </a>	unnamed protein product [synthetic c	<a href="#">50.8</a>	6e-06
<a href="#">gi 15554466 emb CAC69558.1 </a>	unnamed protein product [synthetic c	<a href="#">50.8</a>	6e-06
<a href="#">gi 3990913 gb AAC84340.1 AR000763</a>	Sequence 39 from patent US 573	<a href="#">50.4</a>	7e-06
<a href="#">gi 3990914 gb AAC84341.1 AR000764</a>	Sequence 40 from patent US 573	<a href="#">50.4</a>	7e-06
<a href="#">gi 33759590 gb AAQ52080.1 </a>	Sequence 55 from patent US 6593083...	<a href="#">50.4</a>	9e-06
<a href="#">gi 3990903 gb AAC84330.1 AR000753</a>	Sequence 29 from patent US 573	<a href="#">49.3</a>	2e-05
<a href="#">gi 3990902 gb AAC84329.1 AR000752</a>	Sequence 28 from patent US 573	<a href="#">49.3</a>	2e-05
<a href="#">gi 3990904 gb AAC84331.1 AR000754</a>	Sequence 30 from patent US 573	<a href="#">48.9</a>	2e-05
<a href="#">gi 15554474 emb CAC69562.1 </a>	unnamed protein product [synthetic c	<a href="#">48.9</a>	3e-05
<a href="#">gi 15554478 emb CAC69564.1 </a>	unnamed protein product [synthetic c	<a href="#">48.1</a>	4e-05
<a href="#">gi 83329648 gb ABC06928.1 </a>	Sequence 52 from patent US 6960659	<a href="#">48.1</a>	4e-05
<a href="#">gi 3990915 gb AAC84342.1 AR000765</a>	Sequence 41 from patent US 573	<a href="#">47.8</a>	5e-05
<a href="#">gi 56569106 gb AAV99352.1 </a>	Sequence 272 from patent US 676202...	<a href="#">47.4</a>	7e-05
<a href="#">gi 47255634 gb AAT22908.1 </a>	Sequence 148 from patent US 670982...	<a href="#">47.4</a>	7e-05
<a href="#">gi 492886 emb CAA00808.1 </a>	unnamed protein product [Potato virus	<a href="#">46.2</a>	1e-04
<a href="#">gi 14101400 gb AAE53717.1 </a>	Sequence 70 from patent US 6150087...	<a href="#">46.2</a>	2e-04
<a href="#">gi 14101367 gb AAE53684.1 </a>	Sequence 2 from patent US 6150087 ...	<a href="#">46.2</a>	2e-04
<a href="#">gi 47267560 gb AAT26432.1 </a>	Sequence 65 from patent US 6720166...	<a href="#">45.8</a>	2e-04
<a href="#">gi 15554486 emb CAC69568.1 </a>	unnamed protein product [synthetic c	<a href="#">45.4</a>	2e-04
<a href="#">gi 15554484 emb CAC69567.1 </a>	unnamed protein product [synthetic c	<a href="#">45.4</a>	2e-04
<a href="#">gi 47255607 gb AAT22881.1 </a>	Sequence 121 from patent US 670982...	<a href="#">45.1</a>	3e-04
<a href="#">gi 42668573 gb AAS24361.1 </a>	Sequence 121 from patent US 666738...	<a href="#">45.1</a>	3e-04
<a href="#">gi 33767207 gb AAQ52969.1 </a>	Sequence 13 from patent US 6596476	<a href="#">45.1</a>	3e-04
<a href="#">gi 14101954 gb AAE54271.1 </a>	Sequence 771 from patent US 6150087	<a href="#">45.1</a>	3e-04
<a href="#">gi 15554482 emb CAC69566.1 </a>	unnamed protein product [synthetic c	<a href="#">45.1</a>	4e-04
<a href="#">gi 15554480 emb CAC69565.1 </a>	unnamed protein product [synthetic c	<a href="#">45.1</a>	4e-04
<a href="#">gi 47234811 gb AAT13745.1 </a>	Sequence 53 from patent US 6696281...	<a href="#">44.7</a>	5e-04
<a href="#">gi 1829777 gb AAB44231.1 </a>	Sequence 5 from patent US 5582968	<a href="#">44.3</a>	6e-04
<a href="#">gi 23316923 gb AAN21418.1 </a>	Sequence 18 from patent US 6416946...	<a href="#">44.3</a>	7e-04
<a href="#">gi 3995362 gb AAC88790.1 AR012912</a>	Sequence 7 from patent US 5763	<a href="#">44.3</a>	7e-04
<a href="#">gi 56568990 gb AAV99236.1 </a>	Sequence 103 from patent US 6762024	<a href="#">43.9</a>	7e-04
<a href="#">gi 23315947 gb AAN20959.1 </a>	Sequence 204 from patent US 6413517	<a href="#">43.9</a>	8e-04
<a href="#">gi 56569109 gb AAV99355.1 </a>	Sequence 275 from patent US 6762024	<a href="#">43.5</a>	0.001
<a href="#">gi 3995363 gb AAC88791.1 AR012913</a>	Sequence 8 from patent US 5763	<a href="#">43.5</a>	0.001
<a href="#">gi 7224497 gb AAE24664.1 </a>	Sequence 44 from patent US 5910405	<a href="#">43.5</a>	0.001
<a href="#">gi 47267488 gb AAT26396.1 </a>	Sequence 16 from patent US 6720166...	<a href="#">43.1</a>	0.001
<a href="#">gi 15554464 emb CAC69557.1 </a>	unnamed protein product [synthetic c	<a href="#">42.7</a>	0.002
<a href="#">gi 15554462 emb CAC69556.1 </a>	unnamed protein product [synthetic c	<a href="#">42.7</a>	0.002
<a href="#">gi 56568989 gb AAV99235.1 </a>	Sequence 102 from patent US 6762024	<a href="#">42.4</a>	0.002
<a href="#">gi 2296952 emb CAA02588.1 </a>	unnamed protein product [Hepatitis...	<a href="#">42.4</a>	0.002
<a href="#">gi 23315943 gb AAN20955.1 </a>	Sequence 200 from patent US 6413517	<a href="#">42.4</a>	0.003
<a href="#">gi 2296950 emb CAA02587.1 </a>	unnamed protein product [Hepatitis...	<a href="#">41.6</a>	0.004
<a href="#">gi 6065683 emb CAB58544.1 </a>	unnamed protein product [Dengue virus	<a href="#">41.6</a>	0.004
<a href="#">gi 42685374 gb AAS29955.1 </a>	Sequence 5 from patent US 6680059 ...	<a href="#">41.2</a>	0.005
<a href="#">gi 40160956 gb AAR67308.1 </a>	Sequence 27 from patent US 6635257	<a href="#">41.2</a>	0.005
<a href="#">gi 3990918 gb AAC84345.1 AR000768</a>	Sequence 44 from patent US 573	<a href="#">40.0</a>	0.010
<a href="#">gi 33758793 gb AAQ51732.1 </a>	Sequence 1 from patent US 6592871 ...	<a href="#">39.7</a>	0.013
<a href="#">gi 3990917 gb AAC84344.1 AR000767</a>	Sequence 43 from patent US 573	<a href="#">39.7</a>	0.013
<a href="#">gi 3990916 gb AAC84343.1 AR000766</a>	Sequence 42 from patent US 573	<a href="#">39.7</a>	0.013
<a href="#">gi 33767201 gb AAQ52963.1 </a>	Sequence 7 from patent US 6596476	<a href="#">39.3</a>	0.019
<a href="#">gi 2296962 emb CAA02593.1 </a>	unnamed protein product [Hepatitis...	<a href="#">39.3</a>	0.020
<a href="#">gi 40082535 gb AAR41089.1 </a>	Sequence 4359 from patent US 6605709	<a href="#">39.3</a>	0.021

<a href="#">gi 45503032 emb CAF86306.1 </a>	unnamed protein product [Homo sapien	38.9	0.021
<a href="#">gi 23315942 gb AAN20954.1 </a>	Sequence 199 from patent US 6413517	38.9	0.024
<a href="#">gi 2296958 emb CAA02591.1 </a>	unnamed protein product [Hepatitis...	38.9	0.026
<a href="#">gi 40160955 gb AAR67307.1 </a>	Sequence 26 from patent US 6635257	38.5	0.031
<a href="#">gi 3995364 gb AAC88792.1 AR012914</a>	Sequence 9 from patent US 5763	38.1	0.037
<a href="#">gi 27647036 emb CAD60138.1 </a>	unnamed protein product [Flavivir...	38.1	0.039
<a href="#">gi 2296960 emb CAA02592.1 </a>	unnamed protein product [Hepatitis...	38.1	0.039
<a href="#">gi 40103007 gb AAR48358.1 </a>	Sequence 8075 from patent US 6610836	38.1	0.040
<a href="#">gi 56568984 gb AAV99230.1 </a>	Sequence 97 from patent US 6762024...	38.1	0.041
<a href="#">gi 47255593 gb AAT22867.1 </a>	Sequence 107 from patent US 670982...	38.1	0.041
<a href="#">gi 20224835 gb AAE88376.1 </a>	Sequence 44 from patent US 6335435...	38.1	0.044
<a href="#">gi 20224829 gb AAE88370.1 </a>	Sequence 38 from patent US 6335435...	38.1	0.044
<a href="#">gi 67582840 gb AAV71465.1 </a>	Sequence 1512 from patent US 68874...	37.7	0.050
<a href="#">gi 56627913 gb AAW06247.1 </a>	Sequence 7 from patent US 6797809 ...	37.7	0.061
<a href="#">gi 56568985 gb AAV99231.1 </a>	Sequence 98 from patent US 6762024	37.4	0.070
<a href="#">gi 1829782 gb AAB44236.1 </a>	Sequence 10 from patent US 5582968	37.0	0.086
<a href="#">gi 40160953 gb AAR67305.1 </a>	Sequence 24 from patent US 6635257	37.0	0.095
<a href="#">gi 33741959 gb AAQ42691.1 </a>	Sequence 75 from patent US 6583112	37.0	0.10
<a href="#">gi 5972345 gb AAE12236.1 </a>	Sequence 77 from patent US 5824501 ...	37.0	0.10
<a href="#">gi 23316924 gb AAN21419.1 </a>	Sequence 19 from patent US 6416946...	36.6	0.11
<a href="#">gi 23315996 gb AAN21008.1 </a>	Sequence 253 from patent US 6413517	36.6	0.13
<a href="#">gi 2296956 emb CAA02590.1 </a>	unnamed protein product [Hepatitis...	36.2	0.15
<a href="#">gi 47255579 gb AAT22853.1 </a>	Sequence 93 from patent US 6709828...	35.8	0.19
<a href="#">gi 40192138 gb AAR77444.1 </a>	Sequence 93 from patent US 6649735	35.8	0.19
<a href="#">gi 23316925 gb AAN21420.1 </a>	Sequence 20 from patent US 6416946...	35.8	0.23
<a href="#">gi 91175839 gb ABE26533.1 </a>	Sequence 14 from patent US 7022830...	35.8	0.23
<a href="#">gi 53957550 gb AAV07547.1 </a>	Sequence 19504 from patent US 6747137	35.0	0.33
<a href="#">gi 20224830 gb AAE88371.1 </a>	Sequence 39 from patent US 6335435...	35.0	0.36
<a href="#">gi 5972344 gb AAE12235.1 </a>	Sequence 76 from patent US 5824501 ...	35.0	0.36
<a href="#">gi 59738755 gb AAW92929.1 </a>	Sequence 10492 from patent US 6833447	34.3	0.56
<a href="#">gi 91175841 gb ABE26535.1 </a>	Sequence 16 from patent US 7022830...	34.3	0.67
<a href="#">gi 91175846 gb ABE26540.1 </a>	Sequence 21 from patent US 7022830...	33.5	0.92
<a href="#">gi 42681965 gb AAS28430.1 </a>	Sequence 3572 from patent US 6673910	33.1	1.2
<a href="#">gi 91175843 gb ABE26537.1 </a>	Sequence 18 from patent US 7022830...	33.1	1.3
<a href="#">gi 23315918 gb AAN20930.1 </a>	Sequence 175 from patent US 6413517	33.1	1.3

## Alignments

Get selected sequences

Select all

Deselect all

Distance tree of results

> [gi|594200|gb|AAA55807.1|](#) Sequence 53 from Patent EP 0318216  
[gi|592429|gb|AAA54036.1|](#) Sequence 9 from Patent WO 8904669  
Length=2261

Score = 1303 bits (3372), Expect = 0.0, Method: Composition-based stats.  
Identities = 683/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	402	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	461
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	462	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	521
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	522	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	581



# results of BLAST

BLASTP 2.2.14 [May-07-2006]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

**Reference:**

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153602022-27610-106952644218.BLASTQ1

**Database:** NCBI Protein Reference Sequences

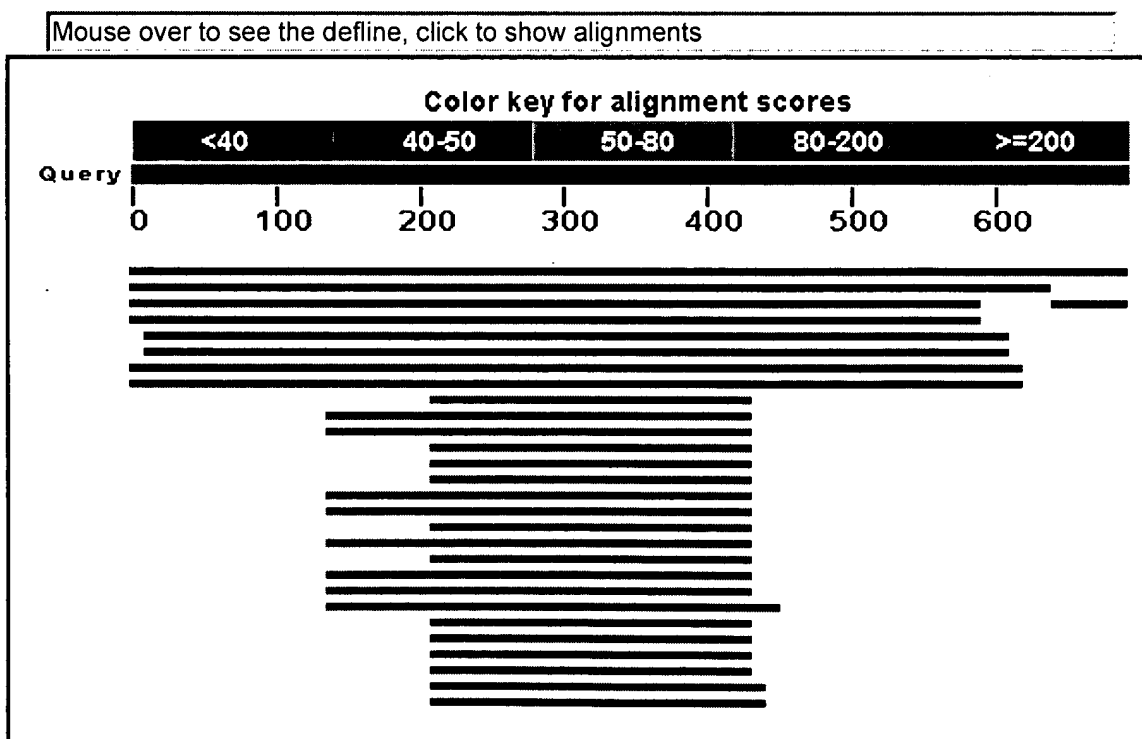
2,389,055 sequences; 864,113,167 total letters

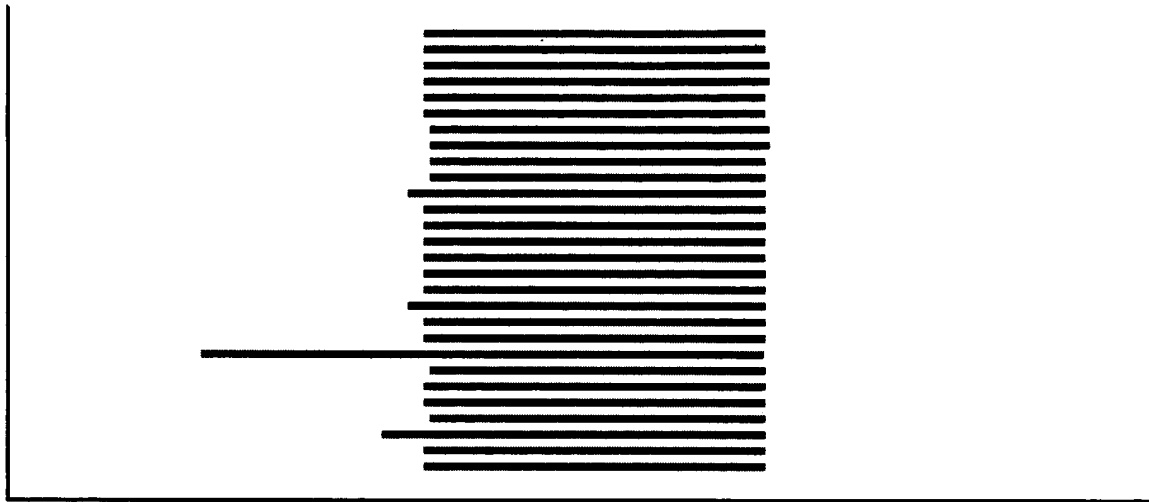
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)  
[Taxonomy reports](#)

**Query=**

Length=685

## Distribution of 100 Blast Hits on the Query Sequence





# Distance tree of results NEW

Sequences producing significant alignments:			Score (Bits)	E Value	
<a href="#">gi 22129793 ref NP_671491.1 </a>	polyprotein [Hepatitis C virus]	<a href="#">1286</a>	0.0	<a href="#">G</a>	
<a href="#">gi 28921568 ref NP_803144.1 </a>	NS3 protease/helicase' [Hepatitis C	<a href="#">1167</a>	0.0	<a href="#">G</a>	
<a href="#">gi 9628102 ref NP_056931.1 </a>	polyprotein [Hepatitis GB virus B]	<a href="#">400</a>	1e-109	<a href="#">G</a>	
<a href="#">gi 26251699 ref NP_757357.1 </a>	putative NS3 proteinase/ATPase/heli	<a href="#">393</a>	8e-108	<a href="#">G</a>	
<a href="#">gi 9628706 ref NP_043570.1 </a>	polyprotein precursor [GB virus C/He	<a href="#">387</a>	8e-106	<a href="#">G</a>	
<a href="#">gi 28971393 ref NP_803205.1 </a>	NS3 proteinase/ATPase/helicase [GB	<a href="#">382</a>	3e-104	<a href="#">G</a>	
<a href="#">gi 9629719 ref NP_045010.1 </a>	polyprotein precursor [Hepatitis GB	<a href="#">359</a>	2e-97	<a href="#">G</a>	
<a href="#">gi 28971401 ref NP_803213.1 </a>	NS3 proteinase/ATPase/helicase [Hep	<a href="#">352</a>	2e-95	<a href="#">G</a>	
<a href="#">gi 26053627 ref NP_751925.1 </a>	NS4A protein [Hepatitis C virus]	<a href="#">85.5</a>	5e-15	<a href="#">G</a>	
<a href="#">gi 9626650 ref NP_040937.1 </a>	polyprotein [Bovine viral diarrhea v	<a href="#">79.7</a>	3e-13	<a href="#">G</a>	
<a href="#">gi 20198946 ref NP_620062.1 </a>	polyprotein [Border disease virus 1	<a href="#">79.3</a>	4e-13	<a href="#">G</a>	
<a href="#">gi 27883894 ref NP_777540.1 </a>	nonstructural protein NS2-3 [Border	<a href="#">79.0</a>	5e-13	<a href="#">G</a>	
<a href="#">gi 27777749 ref NP_776266.1 </a>	nonstructural protein NS2-3 [Bovine	<a href="#">78.6</a>	6e-13	<a href="#">G</a>	
<a href="#">gi 27777750 ref NP_776267.1 </a>	nonstructural protein NS3 [Bovine v	<a href="#">77.8</a>	1e-12	<a href="#">G</a>	
<a href="#">gi 20178631 ref NP_620051.1 </a>	polyprotein [Pestivirus Reindeer-1]	<a href="#">76.6</a>	3e-12	<a href="#">G</a>	
<a href="#">gi 27883895 ref NP_777541.1 </a>	nonstructural protein NS3 [Border d	<a href="#">76.6</a>	3e-12	<a href="#">G</a>	
<a href="#">gi 20178633 ref NP_620053.1 </a>	polyprotein [Pestivirus Giraffe-1]	<a href="#">76.3</a>	3e-12	<a href="#">G</a>	
<a href="#">gi 27885135 ref NP_777514.1 </a>	nonstructural protein NS2-3; NTP...	<a href="#">75.9</a>	4e-12	<a href="#">G</a>	
<a href="#">gi 27885118 ref NP_777527.1 </a>	nonstructural protein NS2-3; NTP...	<a href="#">75.1</a>	8e-12	<a href="#">G</a>	
<a href="#">gi 27885136 ref NP_777515.1 </a>	nonstructural protein NS3; NTPas...	<a href="#">74.3</a>	1e-11	<a href="#">G</a>	
<a href="#">gi 12657942 ref NP_075354.1 </a>	polyprotein [Classical swine fever	<a href="#">74.3</a>	1e-11	<a href="#">G</a>	
<a href="#">gi 27885150 ref NP_777501.1 </a>	nonstructural protein NS2-3 [Classi	<a href="#">73.6</a>	2e-11	<a href="#">G</a>	
<a href="#">gi 27885119 ref NP_777528.1 </a>	nonstructural protein NS3; NTPas...	<a href="#">73.2</a>	3e-11	<a href="#">G</a>	
<a href="#">gi 27885151 ref NP_777502.1 </a>	nonstructural protein NS3 [Classica	<a href="#">71.2</a>	1e-10	<a href="#">G</a>	
<a href="#">gi 9629507 ref NP_044731.1 </a>	putative polyprotein [Bovine viral d	<a href="#">71.2</a>	1e-10	<a href="#">G</a>	
<a href="#">gi 27885409 ref NP_777488.1 </a>	nonstructural protein NS2-3; NTP...	<a href="#">70.9</a>	1e-10	<a href="#">G</a>	
<a href="#">gi 27885410 ref NP_777489.1 </a>	nonstructural protein NS3; NTPas...	<a href="#">69.3</a>	4e-10	<a href="#">G</a>	
<a href="#">gi 9790345 ref NP_062908.1 </a>	polyprotein [Tobacco etch virus]	<a href="#">65.1</a>	8e-09		
<a href="#">gi 25013637 ref NP_734211.1 </a>	CI protein [Tobacco etch virus]	<a href="#">65.1</a>	8e-09	<a href="#">G</a>	

gi 9633629 ref NP_051161.1	polyprotein [Japanese yam mosaic vir	62.8	4e-08	G
gi 25013886 ref NP_734227.1	CI protein [Japanese yam mosaic vir	62.0	6e-08	G
gi 9629731 ref NP_045216.1	polyprotein [Sweet potato feathery m	61.2	1e-07	G
gi 25013777 ref NP_734313.1	CI protein [Sweet potato feathery m	60.5	2e-07	G
gi 21427634 ref NP_659018.1	polyprotein [Cowpea aphid-borne mos	59.7	4e-07	G
gi 25013523 ref NP_734383.1	CI protein [Cowpea aphid-borne mosa	59.7	4e-07	G
gi 45004655 ref NP_982308.1	polyprotein [Chilli veinal mottle v	58.5	7e-07	G
gi 45004660 ref NP_982339.1	cytoplasmic inclusion protein [Chil	58.5	7e-07	G
gi 18677788 ref NP_570723.1	polyprotein [Bean common mosaic vir	57.0	2e-06	G
gi 25013493 ref NP_734117.1	CI protein [Bean common mosaic viru	56.6	3e-06	G
gi 9626509 ref NP_040807.1	polyprotein [Plum pox virus]	56.2	4e-06	G
gi 51949946 ref YP_077181.1	polyprotein [Watermelon mosaic viru	56.2	4e-06	
gi 51949950 ref YP_077271.1	cylindrical inclusion protein [Wate	56.2	4e-06	
gi 56407094 ref NP_062866.2	polyprotein [Turnip mosaic virus]	55.8	4e-06	G
gi 25013653 ref NP_734217.1	CI protein [Turnip mosaic virus]	55.8	4e-06	G
gi 20087055 ref NP_613274.1	polyprotein [Dasheen mosaic virus]	55.8	5e-06	G
gi 25013787 ref NP_734107.1	CI protein [Dasheen mosaic virus]	55.8	5e-06	G
gi 25013583 ref NP_734343.1	CI protein [Plum pox virus]	55.5	6e-06	G
gi 9627035 ref NP_041276.1	polyprotein [Pepper mottle virus]	55.1	9e-06	G
gi 25013572 ref NP_734432.1	CI protein [Pepper mottle virus]	55.1	9e-06	G
gi 9633623 ref NP_051124.1	polyprotein [Murray Valley encephali	53.9	2e-05	G
gi 85677474 ref YP_459919.1	polyprotein [East Asian Passiflora	53.9	2e-05	
gi 25013612 ref NP_734196.1	CI protein [Soybean mosaic virus]	53.5	2e-05	G
gi 12018226 ref NP_072165.1	polyprotein precursor [Soybean mosa	53.5	2e-05	G
gi 21431572 ref NP_659008.1	polyprotein [Potato virus V]	53.1	3e-05	G
gi 71647083 ref YP_271857.1	polyprotein [Wisteria vein mosaic v	53.1	3e-05	
gi 39163615 ref NP_945133.1	polyprotein [Lily mottle virus]	53.1	3e-05	G
gi 39163620 ref NP_945140.1	CI protein [Lily mottle virus]	53.1	3e-05	G
gi 22550316 ref NP_689391.1	polyprotein [Montana myotis leukoen	53.1	3e-05	G
gi 24418986 ref NP_722535.1	NS3; nonstructural protein 3; pr...	53.1	3e-05	G
gi 25013853 ref NP_734373.1	CI protein [Potato virus V]	53.1	3e-05	G
gi 90093257 ref YP_529494.1	CI protein [Konjak mosaic virus]	52.8	4e-05	
gi 90093252 ref YP_529485.1	polyprotein [Konjak mosaic virus]	52.8	4e-05	
gi 27669994 ref NP_775649.1	non-structural protein NS3 [Mont...	52.0	6e-05	G
gi 20153340 ref NP_619667.1	polyprotein [Lettuce mosaic virus]	52.0	8e-05	G
gi 19881395 ref NP_612218.1	polyprotein [Bean yellow mosaic vir	51.6	8e-05	G
gi 25013503 ref NP_734177.1	CI protein [Bean yellow mosaic viru	51.6	8e-05	G
gi 40254028 ref NP_954611.1	polyprotein [Beet mosaic virus]	51.6	9e-05	G
gi 40254033 ref NP_954623.1	CI protein [Beet mosaic virus]	51.6	9e-05	G
gi 25013533 ref NP_734157.1	CI protein [Lettuce mosaic virus]	51.6	9e-05	G
gi 25013916 ref NP_734353.1	CI protein [Bean common mosaic necr	51.6	9e-05	G
gi 21553929 ref NP_660175.1	polyprotein [Bean common mosaic nec	51.6	9e-05	G
gi 20153408 ref NP_619668.1	polyprotein [Johnsongrass mosaic vi	51.2	1e-04	G
gi 25013812 ref NP_734402.1	CI protein [Johnsongrass mosaic vir	51.2	1e-04	G
gi 76803356 ref YP_331413.1	polyprotein [Shallot yellow stripe	50.4	2e-04	
gi 76803355 ref YP_331412.1	polyprotein [Shallot yellow stripe	50.4	2e-04	
gi 76803361 ref YP_331418.1	CI protein [Shallot yellow stripe v	50.4	2e-04	
gi 20428637 ref NP_620483.1	polyprotein [Cocksfoot streak virus	50.4	2e-04	G

<a href="#">gi 25014042 ref NP_734393.1 </a>	CI protein [Cocksfoot streak virus]	<a href="#">50.1</a>	2e-04	<a href="#">G</a>
<a href="#">gi 17059638 ref NP_477522.1 </a>	polyprotein [Zucchini yellow mosaic	<a href="#">50.1</a>	2e-04	<a href="#">G</a>
<a href="#">gi 25013663 ref NP_734187.1 </a>	CI protein [Zucchini yellow mosaic	<a href="#">50.1</a>	2e-04	<a href="#">G</a>
<a href="#">gi 48843533 ref YP_025107.1 </a>	polyprotein [Hordeum mosaic virus]	<a href="#">50.1</a>	3e-04	<a href="#">G</a>
<a href="#">gi 20087031 ref NP_613273.1 </a>	polyprotein [Clover yellow vein vir	<a href="#">49.3</a>	4e-04	<a href="#">G</a>
<a href="#">gi 25013513 ref NP_734167.1 </a>	CI protein [Clover yellow vein viru	<a href="#">49.3</a>	4e-04	<a href="#">G</a>
<a href="#">gi 9626461 ref NP_059434.1 </a>	hypothetical protein JEVgpl [Japanes	<a href="#">49.3</a>	5e-04	<a href="#">G</a>
<a href="#">gi 51101432 ref YP_063390.1 </a>	CI protein [Hordeum mosaic virus]	<a href="#">48.9</a>	6e-04	<a href="#">G</a>
<a href="#">gi 27696332 ref NP_775670.1 </a>	non-structural protein NS3 [Japanes	<a href="#">48.5</a>	7e-04	<a href="#">G</a>
<a href="#">gi 56692442 ref YP_164264.1 </a>	polyprotein precursor [Usutu virus]	<a href="#">48.5</a>	8e-04	
<a href="#">gi 21492612 ref NP_659729.1 </a>	polyprotein [Potato virus A]	<a href="#">48.1</a>	0.001	<a href="#">G</a>
<a href="#">gi 25013593 ref NP_734363.1 </a>	CI protein [Potato virus A]	<a href="#">48.1</a>	0.001	<a href="#">G</a>
<a href="#">gi 9627243 ref NP_041725.1 </a>	cell fusing agent polyprotein [Cell	<a href="#">48.1</a>	0.001	<a href="#">G</a>
<a href="#">gi 9626682 ref NP_056776.1 </a>	hypothetical protein DENVgpl [Dengue	<a href="#">47.8</a>	0.001	<a href="#">G</a>
<a href="#">gi 27366084 ref NP_761612.1 </a>	HrpA-like helicase [Vibrio vulnific	<a href="#">47.8</a>	0.001	<a href="#">G</a>
<a href="#">gi 25059134 ref NP_739587.1 </a>	NS3 protein [Dengue virus type 2]	<a href="#">47.8</a>	0.001	<a href="#">G</a>
<a href="#">gi 37679649 ref NP_934258.1 </a>	HrpA-like helicase [Vibrio vulnific	<a href="#">47.4</a>	0.002	<a href="#">G</a>
<a href="#">gi 56692450 ref YP_164814.1 </a>	NS3 [Usutu virus]	<a href="#">47.4</a>	0.002	
<a href="#">gi 9629497 ref NP_044727.1 </a>	polyprotein [Ryegrass mosaic virus]	<a href="#">47.4</a>	0.002	<a href="#">G</a>
<a href="#">gi 9628430 ref NP_056765.1 </a>	polyprotein [Pea seed-borne mosaic v	<a href="#">47.4</a>	0.002	<a href="#">G</a>
<a href="#">gi 25013563 ref NP_734423.1 </a>	CI protein [Pea seed-borne mosaic v	<a href="#">47.0</a>	0.002	<a href="#">G</a>
<a href="#">gi 18652417 ref NP_570725.1 </a>	polyprotein [Scallion mosaic virus]	<a href="#">47.0</a>	0.002	<a href="#">G</a>
<a href="#">gi 25014000 ref NP_734127.1 </a>	CI protein [Scallion mosaic virus]	<a href="#">47.0</a>	0.002	<a href="#">G</a>
<a href="#">gi 25013863 ref NP_734323.1 </a>	CI protein [Ryegrass mosaic virus]	<a href="#">47.0</a>	0.002	<a href="#">G</a>
<a href="#">gi 20177456 ref NP_619758.1 </a>	polyprotein [Modoc virus]	<a href="#">46.6</a>	0.003	<a href="#">G</a>
<a href="#">gi 48237788 ref YP_022751.1 </a>	polyprotein [Yam mosaic virus]	<a href="#">46.2</a>	0.003	<a href="#">G</a>
<a href="#">gi 33620714 ref NP_891560.1 </a>	polyprotein precursor [Kamiti River	<a href="#">46.2</a>	0.003	<a href="#">G</a>
<a href="#">gi 27735345 ref NP_776044.1 </a>	putative non-structural protein NS3	<a href="#">46.2</a>	0.003	<a href="#">G</a>
<a href="#">gi 25013602 ref NP_734246.1 </a>	CI protein [Potato virus Y]	<a href="#">46.2</a>	0.003	<a href="#">G</a>
<a href="#">gi 9627729 ref NP_056759.1 </a>	polyprotein [Potato virus Y]	<a href="#">46.2</a>	0.003	<a href="#">G</a>
<a href="#">gi 20178609 ref NP_620044.1 </a>	polyprotein [Rio Bravo virus]	<a href="#">46.2</a>	0.004	<a href="#">G</a>
<a href="#">gi 25013641 ref NP_734331.1 </a>	CI protein [Tobacco vein mottling v	<a href="#">46.2</a>	0.004	<a href="#">G</a>
<a href="#">gi 9629180 ref NP_056867.1 </a>	polyprotein [Tobacco vein mottling v	<a href="#">46.2</a>	0.004	<a href="#">G</a>
<a href="#">gi 28492879 ref NP_787937.1 </a>	polyprotein [Peru tomato mosaic vir	<a href="#">46.2</a>	0.004	<a href="#">G</a>
<a href="#">gi 28519945 ref NP_787942.1 </a>	CI protein [Peru tomato mosaic viru	<a href="#">46.2</a>	0.004	<a href="#">G</a>
<a href="#">gi 48249201 ref YP_022756.1 </a>	CI protein [Yam mosaic virus]	<a href="#">45.8</a>	0.004	<a href="#">G</a>
<a href="#">gi 20070096 ref NP_612585.1 </a>	polyprotein [Brome streak mosaic vi	<a href="#">45.8</a>	0.004	<a href="#">G</a>
<a href="#">gi 25013906 ref NP_734257.1 </a>	CI protein [Brome streak mosaic vir	<a href="#">45.8</a>	0.004	<a href="#">G</a>
<a href="#">gi 27735367 ref NP_776076.1 </a>	non-structural protein NS3 [Rio Bra	<a href="#">45.4</a>	0.006	<a href="#">G</a>
<a href="#">gi 12084823 ref NP_073286.1 </a>	polyprotein precursor [Dengue virus	<a href="#">45.4</a>	0.006	
<a href="#">gi 9626684 ref NP_040961.1 </a>	hypothetical protein [Dengue virus t	<a href="#">45.4</a>	0.006	
<a href="#">gi 73671175 ref NP_740321.1 </a>	NS3 protein [Dengue virus type 4]	<a href="#">45.1</a>	0.007	
<a href="#">gi 37695586 ref NP_937777.1 </a>	NS3 protein [Kamiti River virus]	<a href="#">45.1</a>	0.008	<a href="#">G</a>
<a href="#">gi 25121728 ref NP_740264.1 </a>	non-structural protein 3 [Modoc vir	<a href="#">45.1</a>	0.008	<a href="#">G</a>
<a href="#">gi 9627245 ref NP_041726.1 </a>	polyprotein precursor [Yellow fever	<a href="#">44.7</a>	0.011	
<a href="#">gi 15595172 ref NP_212961.1 </a>	ATP-dependent helicase (hrpA) [Borr	<a href="#">44.7</a>	0.012	<a href="#">G</a>
<a href="#">gi 68299604 ref YP_249455.1 </a>	polyprotein [Pennisetum mosaic viru	<a href="#">44.3</a>	0.013	
<a href="#">gi 88861126 ref ZP_01135760.1 </a>	ATP-dependent DNA helicase [Pseud	<a href="#">44.3</a>	0.015	

gi 25140981 ref NP_741959.1	polyprotein [Wild potato mosaic vir	43.9	0.016	G
gi 76650592 ref XP_885404.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650590 ref XP_885374.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650588 ref XP_885353.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650586 ref XP_885324.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650584 ref XP_582847.2	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650582 ref XP_885275.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650576 ref XP_872459.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 27735293 ref NP_776005.1	non-structural protein NS3 [Yellow	43.9	0.017	G
gi 50944385 ref XP_481720.1	RNA helicase-like [Oryza sativa (ja	43.9	0.017	U G
gi 47059171 ref NP_997661.1	DEAH (Asp-Glu-Ala-His) box polypept	43.9	0.020	U G
gi 30794426 ref NP_081263.1	DEAH (Asp-Glu-Ala-His) box polypept	43.9	0.020	U G
gi 25141242 ref NP_741973.1	CI protein [Wild potato mosaic viru	43.5	0.024	G
gi 27383239 ref NP_774768.1	helicase [Bradyrhizobium japonicum	43.1	0.028	G
gi 20178607 ref NP_620045.1	polyprotein [Apoi virus]	43.1	0.029	G
gi 4503293 ref NP_003578.1	DEAH (Asp-Glu-Ala-His) box polypepti	43.1	0.030	U G
gi 108860675 ref NP_001035839.1	DEAH (Asp-Glu-Ala-His) box poly	43.1	0.030	G
gi 73972117 ref XP_856831.1	PREDICTED: similar to Putative p...	43.1	0.033	G
gi 73972115 ref XP_856794.1	PREDICTED: similar to Putative p...	43.1	0.033	G
gi 73972113 ref XP_856752.1	PREDICTED: similar to Putative p...	43.1	0.033	G
gi 73972109 ref XP_538827.2	PREDICTED: similar to Putative p...	43.1	0.033	G
gi 11528014 ref NP_041724.2	polyprotein precursor [West Nile vi	43.1	0.035	G
gi 71077358 ref XP_771193.1	Giardia lamblia ATCC 50803 pre-m...	42.7	0.036	G
gi 9626686 ref NP_059433.1	polyprotein [Dengue virus type 1]	42.7	0.036	
gi 22329903 ref NP_174527.2	EMB2733; ATP binding / ATP-depen...	42.7	0.039	U G
gi 51599078 ref YP_073266.1	ATP-dependent helicase [Borrelia ga	42.7	0.040	G
gi 27735306 ref NP_776018.1	non-structural protein NS3 [West Ni	42.7	0.041	G
gi 25014066 ref NP_722463.1	nonstructural protein 3 [Dengue vir	42.7	0.041	
gi 18652415 ref NP_570724.1	polyprotein [Sugarcane mosaic virus	42.4	0.052	G
gi 18490053 ref NP_569138.1	polyprotein [Maize dwarf mosaic vir	42.4	0.059	G
gi 19112478 ref NP_595686.1	hypothetical protein SPBC19C2.01...	42.0	0.067	G
gi 76650580 ref XP_885249.1	PREDICTED: similar to Putative p...	42.0	0.073	G
gi 96980661 ref YP_610949.1	polyprotein [Daphne virus Y]	42.0	0.076	
gi 96980666 ref YP_611115.1	CI protein [Daphne virus Y]	41.6	0.085	
gi 69950831 ref ZP_00638649.1	ATP-dependent helicase HrpB [S...	41.6	0.090	
gi 86147501 ref ZP_01065812.1	putative ATP-dependent helicase [	41.6	0.093	
gi 25013543 ref NP_734147.1	CI (cytoplasmic inclusion) protein	41.6	0.097	G
gi 25013623 ref NP_734137.1	CI protein [Sugarcane mosaic virus]	41.2	0.10	G
gi 84391226 ref ZP_00991557.1	putative ATP-dependent helicase [	41.2	0.11	
gi 91786081 ref YP_547033.1	ATP-dependent DNA helicase RecQ [Po	41.2	0.11	G
gi 73972111 ref XP_856707.1	PREDICTED: similar to Putative p...	41.2	0.11	G
gi 110595523 ref ZP_01383854.1	ATP-dependent DNA helicase, R...	41.2	0.11	
gi 27697401 ref NP_775684.1	non-structural protein NS3 [Apoi vi	41.2	0.12	G
gi 83648495 ref YP_436930.1	ATP-dependent helicase HrpB [Hahell	40.8	0.14	G
gi 77953536 ref ZP_00817943.1	ATP-dependent helicase HrpB [Mari	40.4	0.19	
gi 24642763 ref NP_573208.1	CG8915-PA [Drosophila melanogaster]	40.4	0.20	U G
gi 83815480 ref YP_446839.1	ATP-dependent helicase HrpB [Salini	40.4	0.21	G
gi 42569631 ref NP_181077.2	ATP binding / ATP-dependent RNA ...	40.4	0.22	U G

<a href="#">gi 21449931 ref NP_659391.1 </a>	polyprotein [Sorghum mosaic virus]	<a href="#">40.4</a>	0.22	<b>G</b>
<a href="#">gi 47574071 ref ZP_00244108.1 </a>	COG0514: Superfamily II DNA he...	<a href="#">40.4</a>	0.22	
<a href="#">gi 25013836 ref NP_734413.1 </a>	CI protein [Peanut mottle virus]	<a href="#">40.4</a>	0.22	<b>G</b>
<a href="#">gi 15808064 ref NP_068348.2 </a>	polyprotein [Peanut mottle virus]	<a href="#">40.4</a>	0.22	<b>G</b>
<a href="#">gi 25013826 ref NP_734087.1 </a>	CI protein [Sorghum mosaic virus]	<a href="#">40.0</a>	0.27	<b>G</b>
<a href="#">gi 37651480 ref NP_932608.1 </a>	polyprotein [Oat necrotic mottle vi	<a href="#">39.7</a>	0.32	<b>G</b>
<a href="#">gi 38304205 ref NP_940826.1 </a>	CI protein [Oat necrotic mottle vir	<a href="#">39.7</a>	0.32	<b>G</b>
<a href="#">gi 32490549 ref NP_870995.1 </a>	polyprotein [Papaya leaf-distortion	<a href="#">39.7</a>	0.33	<b>G</b>
<a href="#">gi 32493282 ref NP_871732.1 </a>	CI [Papaya leaf-distortion mosaic p	<a href="#">39.7</a>	0.33	<b>G</b>
<a href="#">gi 89362514 ref ZP_01200321.1 </a>	ATP-dependent helicase HrpB [Xant	<a href="#">39.7</a>	0.33	
<a href="#">gi 75209551 ref ZP_00709772.1 </a>	COG0514: Superfamily II DNA helic	<a href="#">39.7</a>	0.33	
<a href="#">gi 50931311 ref XP_475183.1 </a>	putative DEAD/DEAH RNA helicase ...	<a href="#">39.7</a>	0.36	<b>G</b>
<a href="#">gi 24432114 ref NP_722551.1 </a>	polyprotein [Alkhurma virus]	<a href="#">39.7</a>	0.37	<b>G</b>
<a href="#">gi 33112011 ref NP_872627.1 </a>	polyprotein [Yokose virus]	<a href="#">39.3</a>	0.42	<b>G</b>
<a href="#">gi 27545511 ref NP_775474.1 </a>	non-structural protein NS3 [Alkhurm	<a href="#">39.3</a>	0.43	<b>G</b>
<a href="#">gi 33589254 ref NP_878909.1 </a>	polyprotein [Omsk hemorrhagic fever	<a href="#">39.3</a>	0.44	<b>G</b>
<a href="#">gi 9629245 ref NP_056758.1 </a>	polyprotein [Papaya ringspot virus]	<a href="#">39.3</a>	0.46	<b>G</b>
<a href="#">gi 25013553 ref NP_734237.1 </a>	CI protein [Papaya ringspot virus]	<a href="#">39.3</a>	0.46	<b>G</b>
<a href="#">gi 109471230 ref XP_001068289.1 </a>	PREDICTED: similar to DEAH (...)	<a href="#">39.3</a>	0.47	<b>G</b>
<a href="#">gi 9630316 ref NP_046741.1 </a>	polyprotein [Wheat streak mosaic vir	<a href="#">39.3</a>	0.49	<b>G</b>
<a href="#">gi 25013803 ref NP_734269.1 </a>	CI protein [Wheat streak mosaic vir	<a href="#">39.3</a>	0.49	<b>G</b>
<a href="#">gi 6322772 ref NP_012845.1 </a>	Predominantly nucleolar DEAH-box ...	<a href="#">39.3</a>	0.49	<b>G</b>
<a href="#">gi 53715360 ref YP_101352.1 </a>	ATP-dependent DNA helicase RecQ ...	<a href="#">39.3</a>	0.50	<b>G</b>
<a href="#">gi 51242947 ref NP_001003715.1 </a>	RecQ protein-like 5 isoform 2 [H	<a href="#">38.9</a>	0.52	<b>U/G</b>
<a href="#">gi 84995412 ref XP_952428.1 </a>	ATP-dependent helicase [Theileria a	<a href="#">38.9</a>	0.53	<b>G</b>
<a href="#">gi 51242943 ref NP_001003716.1 </a>	RecQ protein-like 5 isoform 3 [H	<a href="#">38.9</a>	0.55	<b>U/G</b>
<a href="#">gi 71838030 ref ZP_00677792.1 </a>	ATP-dependent helicase HrpB [Pelo	<a href="#">38.9</a>	0.56	
<a href="#">gi 20522133 ref NP_620656.1 </a>	polyprotein [Sweet potato mild mott	<a href="#">38.9</a>	0.58	<b>G</b>
<a href="#">gi 25013876 ref NP_734287.1 </a>	CI protein [Sweet potato mild mottl	<a href="#">38.9</a>	0.59	<b>G</b>
<a href="#">gi 21919420 ref NP_665685.1 </a>	DEAH (Asp-Glu-Ala-His) box polypept	<a href="#">38.9</a>	0.63	<b>U/G</b>
<a href="#">gi 90419404 ref ZP_01227314.1 </a>	putative ATP-dependent DNA helica	<a href="#">38.9</a>	0.64	
<a href="#">gi 42525842 ref NP_970940.1 </a>	ATP-dependent DNA helicase RecQ ...	<a href="#">38.5</a>	0.68	<b>G</b>
<a href="#">gi 37559066 ref NP_932089.1 </a>	non-structural protein NS3 [Omsk he	<a href="#">38.5</a>	0.70	<b>G</b>
<a href="#">gi 58264732 ref XP_569522.1 </a>	pre-mRNA splicing factor [Crypto...	<a href="#">38.5</a>	0.71	<b>G</b>
<a href="#">gi 78692610 ref ZP_00857124.1 </a>	ATP-dependent DNA helicase Rec...	<a href="#">38.5</a>	0.76	
<a href="#">gi 71675635 ref ZP_00673379.1 </a>	ATP-dependent DNA helicase Rec...	<a href="#">38.5</a>	0.78	
<a href="#">gi 88810592 ref ZP_01125849.1 </a>	Lhr-like helicase [Nitrococcus mo	<a href="#">38.5</a>	0.82	
<a href="#">gi 32490547 ref NP_871002.1 </a>	polyprotein [Onion yellow dwarf vir	<a href="#">38.5</a>	0.83	<b>G</b>
<a href="#">gi 32493292 ref NP_871742.1 </a>	CI protein [Onion yellow dwarf viru	<a href="#">38.5</a>	0.83	<b>G</b>
<a href="#">gi 78368935 ref ZP_00839126.1 </a>	ATP-dependent helicase HrpB [Shew	<a href="#">38.5</a>	0.83	
<a href="#">gi 88806214 ref ZP_01121732.1 </a>	putative ATP-dependent DNA hel...	<a href="#">38.5</a>	0.86	
<a href="#">gi 53714294 ref YP_100286.1 </a>	hypothetical protein BF3005 [Bacter	<a href="#">38.1</a>	0.92	<b>G</b>
<a href="#">gi 95930623 ref ZP_01313357.1 </a>	ATP-dependent helicase HrpB [D...	<a href="#">38.1</a>	0.93	
<a href="#">gi 76258862 ref ZP_00766515.1 </a>	Aldehyde oxidase and xanthine ...	<a href="#">38.1</a>	0.94	
<a href="#">gi 56480445 ref NP_709628.2 </a>	ATP-dependent DNA helicase [Shig...	<a href="#">38.1</a>	0.97	<b>G</b>
<a href="#">gi 15804414 ref NP_290454.1 </a>	ATP-dependent DNA helicase [Esch...	<a href="#">38.1</a>	1.1	<b>G</b>
<a href="#">gi 49176420 ref YP_026263.1 </a>	ATP-dependent DNA helicase [Esch...	<a href="#">38.1</a>	1.1	<b>G</b>
<a href="#">gi 82546173 ref YP_410120.1 </a>	ATP-dependent DNA helicase [Shigell	<a href="#">38.1</a>	1.1	<b>G</b>
<a href="#">gi 82778997 ref YP_405346.1 </a>	ATP-dependent DNA helicase [Shigell	<a href="#">38.1</a>	1.1	<b>G</b>

gi 75236871 ref ZP_00720940.1	COG0514: Superfamily II DNA helic	38.1	1.1	
gi 75230783 ref ZP_00717246.1	COG0514: Superfamily II DNA helic	38.1	1.1	
gi 83858641 ref ZP_00952163.1	DEAD/DEAH box helicase [Oceanica	38.1	1.1	
gi 90581058 ref ZP_01236858.1	putative ATP-dependent DNA helica	38.1	1.1	
gi 89074461 ref ZP_01160938.1	putative ATP-dependent DNA hel...	38.1	1.1	
gi 77813211 ref ZP_00812489.1	ATP-dependent helicase HrpB [Shew	38.1	1.1	
gi 83954472 ref ZP_00963183.1	ATP-dependent helicase HrpB [Sulf	38.1	1.1	
gi 83943900 ref ZP_00956357.1	ATP-dependent helicase HrpB [Sulf	37.7	1.2	
gi 62182427 ref YP_218844.1	ATP-dependent DNA helicase [Salm...	37.7	1.2	G
gi 56415812 ref YP_152887.1	ATP-dependent DNA helicase [Salm...	37.7	1.2	G
gi 16762176 ref NP_457793.1	ATP-dependent DNA helicase [Salm...	37.7	1.2	G
gi 54310561 ref YP_131581.1	putative ATP-dependent DNA helic...	37.7	1.2	G
gi 109118220 ref XP_001097819.1	PREDICTED: RecQ protein-like 5	37.7	1.2	G
gi 51242949 ref NP_004250.3	RecQ protein-like 5 isoform 1 [Homo	37.7	1.2	U/G
gi 25013749 ref NP_734295.1	CI protein [Barley mild mosaic viru	37.7	1.2	G
gi 19749339 ref NP_604491.1	RNA1 polyprotein [Barley mild mosai	37.7	1.2	G
gi 109118218 ref XP_001098200.1	PREDICTED: RecQ protein-like...	37.7	1.3	G
gi 77361487 ref YP_341062.1	ATP-dependent DNA helicase [Pseu...	37.7	1.3	G
gi 16767228 ref NP_462843.1	ATP-dependent DNA helicase [Salmone	37.7	1.3	G
gi 85000727 ref XP_955082.1	DEAD-box family helicase [Theileria	37.7	1.3	G
gi 72153274 ref XP_787603.1	PREDICTED: similar to DEAH (Asp-...	37.7	1.4	G
gi 67539314 ref XP_663431.1	hypothetical protein AN5827.2 [Aspe	37.7	1.4	G
gi 24646066 ref NP_524319.2	mutagen-sensitive 309 CG6920-PA [Dr	37.4	1.6	U/G
gi 90589729 ref ZP_01245378.1	ATP-dependent DNA helicase Rec...	37.4	1.6	
gi 90414260 ref ZP_01222240.1	putative ATP-dependent DNA hel...	37.4	1.6	
gi 68542893 ref ZP_00582614.1	ATP-dependent helicase HrpB [Shew	37.4	1.6	
gi 82741698 ref ZP_00904413.1	ATP-dependent helicase HrpB [Shew	37.4	1.7	
gi 68545749 ref ZP_00585299.1	ATP-dependent helicase HrpB [Shew	37.4	1.7	
gi 83857591 ref ZP_00951119.1	putative ATP-dependent DNA hel...	37.4	1.7	
gi 83585931 ref ZP_00924570.1	COG0514: Superfamily II DNA helic	37.4	1.7	
gi 58393124 ref XP_319843.2	ENSANGP00000025250 [Anopheles gambi	37.4	1.7	G
gi 24372223 ref NP_716265.1	ATP-dependent helicase HrpB [Shewan	37.4	1.8	G
gi 50123092 ref YP_052259.1	ATP-dependent DNA helicase [Erwi...	37.4	1.8	G
gi 21224937 ref NP_630716.1	ATP-dependent helicase [Streptomyce	37.4	1.8	G
gi 89889904 ref ZP_01201415.1	ATP-dependent DNA helicase RecQ [	37.4	1.8	
gi 91226497 ref ZP_01261246.1	putative ATP-dependent helicase [	37.4	1.9	
gi 109896583 ref YP_659838.1	ATP-dependent DNA helicase RecQ...	37.4	1.9	G
gi 29349252 ref NP_812755.1	ATP-dependent DNA helicase recQ ...	37.0	2.0	G
gi 75188564 ref ZP_00701831.1	COG0514: Superfamily II DNA helic	37.0	2.0	
gi 75853732 ref ZP_00761505.1	COG1643: HrpA-like helicases [Vib	37.0	2.0	
gi 17556386 ref NP_497420.1	Y67D2.6 [Caenorhabditis elegans]	37.0	2.1	U/G
gi 88803234 ref ZP_01118760.1	putative ATP-dependent DNA hel...	37.0	2.1	
gi 89894700 ref YP_518187.1	hypothetical protein DSY1954 [Desul	37.0	2.1	G
gi 71023321 ref XP_761890.1	hypothetical protein UM05743.1 [Ust	37.0	2.2	G
gi 77360909 ref YP_340484.1	ATP-dependent helicase with nucl...	37.0	2.3	G
gi 86140388 ref ZP_01058947.1	putative ATP-dependent DNA helica	37.0	2.3	
gi 76638750 ref XP_607648.2	PREDICTED: similar to DEAH (Asp-...	37.0	2.4	G
gi 86133525 ref ZP_01052107.1	putative ATP-dependent DNA helica	37.0	2.4	
gi 66809201 ref XP_638323.1	hypothetical protein DDB0186395 [Di	37.0	2.4	G
gi 67469003 ref XP_650493.1	DEAD/DEAH box helicase [Entamoeba h	37.0	2.5	G
gi 109896817 ref YP_660072.1	ATP-dependent helicase HrpB [Pseud	37.0	2.5	G
gi 109092044 ref XP_001088680.1	PREDICTED: DEAH (Asp-Glu-Ala...	37.0	2.5	G

<a href="#">gi 50423857 ref XP_460513.1 </a>	hypothetical protein DEHA0F03762...	<a href="#">37.0</a>	2.5	<b>G</b>
<a href="#">gi 107026746 ref YP_624257.1 </a>	amidophosphoribosyltransferase ...	<a href="#">37.0</a>	2.5	<b>G</b>
<a href="#">gi 74014888 ref ZP_00685516.1 </a>	Amidophosphoribosyl transferase [	<a href="#">37.0</a>	2.5	
<a href="#">gi 71676318 ref ZP_00674060.1 </a>	Helicase, C-terminal:Type III ...	<a href="#">36.6</a>	2.6	
<a href="#">gi 67547355 ref ZP_00425259.1 </a>	Amidophosphoribosyl transferase [	<a href="#">36.6</a>	2.6	
<a href="#">gi 85713431 ref ZP_01044421.1 </a>	ATP-dependent helicase HrpB [Nitr	<a href="#">36.6</a>	2.6	
<a href="#">gi 67468457 ref XP_650264.1 </a>	recQ family helicase [Entamoeba his	<a href="#">36.6</a>	2.6	<b>G</b>
<a href="#">gi 73965025 ref XP_540436.2 </a>	PREDICTED: similar to ATP-depend...	<a href="#">36.6</a>	2.6	<b>U/G</b>
<a href="#">gi 72161116 ref YP_288773.1 </a>	helicase, C-terminal:DEAD/DEAH b...	<a href="#">36.6</a>	2.7	<b>G</b>
<a href="#">gi 88859956 ref ZP_01134595.1 </a>	putative ATP-dependent helicase [	<a href="#">36.6</a>	2.7	
<a href="#">gi 90592069 ref ZP_01247706.1 </a>	ATP-dependent DNA helicase Rec...	<a href="#">36.6</a>	2.7	
<a href="#">gi 18485510 ref NP_569721.1 </a>	RecQ protein-like 5 [Mus musculus]	<a href="#">36.6</a>	2.8	<b>U/G</b>
<a href="#">gi 90407207 ref ZP_01215394.1 </a>	putative ATP-dependent DNA hel...	<a href="#">36.6</a>	2.8	
<a href="#">gi 20544129 ref NP_068750.2 </a>	DEAH (Asp-Glu-Ala-His) box polypept	<a href="#">36.6</a>	2.9	<b>U/G</b>
<a href="#">gi 84716398 ref ZP_01023028.1 </a>	ATP-dependent DNA helicase Rec...	<a href="#">36.6</a>	2.9	
<a href="#">gi 109492252 ref XP_001081701.1 </a>	PREDICTED: similar to RecQ p...	<a href="#">36.6</a>	2.9	<b>G</b>
<a href="#">gi 17552054 ref NP_498895.1 </a>	RNA HelicAse family member (rha-2)	<a href="#">36.6</a>	3.0	<b>U/G</b>
<a href="#">gi 88792832 ref ZP_01108550.1 </a>	ATP-dependent DNA helicase [Al...	<a href="#">36.6</a>	3.1	
<a href="#">gi 91974782 ref YP_567441.1 </a>	ATP-dependent helicase HrpB [Rhodop	<a href="#">36.6</a>	3.1	<b>G</b>
<a href="#">gi 76645937 ref XP_603974.2 </a>	PREDICTED: similar to ATP-depend...	<a href="#">36.6</a>	3.2	<b>G</b>
<a href="#">gi 78062965 ref YP_372873.1 </a>	amidophosphoribosyltransferase [Bur	<a href="#">36.6</a>	3.3	<b>G</b>
<a href="#">gi 89890375 ref ZP_01201885.1 </a>	ATP-dependent DNA helicase RecQ [	<a href="#">36.6</a>	3.3	
<a href="#">gi 37522198 ref NP_925575.1 </a>	ATP-dependent DNA helicase [Gloeoba	<a href="#">36.2</a>	3.5	<b>G</b>
<a href="#">gi 23004116 ref ZP_00047615.1 </a>	COG0514: Superfamily II DNA he...	<a href="#">36.2</a>	3.6	
<a href="#">gi 94312259 ref YP_585469.1 </a>	ATP-dependent DNA helicase RecQ [Ra	<a href="#">36.2</a>	3.7	<b>G</b>
<a href="#">gi 19074102 ref NP_584708.1 </a>	ATP-DEPENDENT RNA HELICASE (DEAD...	<a href="#">36.2</a>	3.7	<b>G</b>
<a href="#">gi 69951291 ref ZP_00639032.1 </a>	ATP-dependent DNA helicase Rec...	<a href="#">36.2</a>	3.8	
<a href="#">gi 75674557 ref YP_316978.1 </a>	ATP-dependent helicase HrpB [Nitrob	<a href="#">35.8</a>	4.4	<b>G</b>
<a href="#">gi 86148265 ref ZP_01066561.1 </a>	ATP-dependent DNA helicase RecQ [	<a href="#">35.8</a>	4.4	
<a href="#">gi 84393647 ref ZP_00992398.1 </a>	ATP-dependent DNA helicase RecQ [	<a href="#">35.8</a>	4.4	
<a href="#">gi 85014143 ref XP_955567.1 </a>	pre-mRNA splicing factor [Encephali	<a href="#">35.8</a>	4.7	<b>G</b>
<a href="#">gi 56461347 ref YP_156628.1 </a>	Helicase, ATP-dependent [Idiomarina	<a href="#">35.8</a>	4.7	<b>G</b>
<a href="#">gi 55652443 ref XP_514647.1 </a>	PREDICTED: hypothetical protein XP_	<a href="#">35.8</a>	4.7	<b>G</b>
<a href="#">gi 109645079 ref ZP_01368999.1 </a>	DEAD/DEAH box helicase-like [...	<a href="#">35.8</a>	4.7	
<a href="#">gi 77814563 ref ZP_00813821.1 </a>	ATP-dependent DNA helicase Rec...	<a href="#">35.8</a>	4.8	
<a href="#">gi 71000850 ref XP_755106.1 </a>	mRNA splicing factor RNA helicase...	<a href="#">35.8</a>	4.9	<b>G</b>
<a href="#">gi 88713743 ref ZP_01107824.1 </a>	ATP-dependent DNA helicase rec...	<a href="#">35.8</a>	5.0	
<a href="#">gi 54310256 ref YP_131276.1 </a>	hypothetical ATP-dependent helic...	<a href="#">35.8</a>	5.1	<b>G</b>
<a href="#">gi 72109102 ref XP_783015.1 </a>	PREDICTED: similar to Probable A...	<a href="#">35.8</a>	5.1	<b>G</b>
<a href="#">gi 77739558 ref ZP_00808049.1 </a>	ATP-dependent DNA helicase Rec...	<a href="#">35.8</a>	5.2	
<a href="#">gi 58382418 ref XP_311930.2 </a>	ENSANGP00000010973 [Anopheles gambi	<a href="#">35.8</a>	5.3	<b>G</b>
<a href="#">gi 85099496 ref XP_960795.1 </a>	hypothetical protein [Neurospora cr	<a href="#">35.8</a>	5.3	<b>G</b>
<a href="#">gi 86747631 ref YP_484127.1 </a>	ATP-dependent helicase HrpB [Rhodop	<a href="#">35.8</a>	5.4	<b>G</b>
<a href="#">gi 90579760 ref ZP_01235569.1 </a>	putative ATP-dependent helicase [	<a href="#">35.8</a>	5.5	
<a href="#">gi 77952760 ref ZP_00817173.1 </a>	Helicase, C-terminal:DEAD/DEAH...	<a href="#">35.8</a>	5.5	
<a href="#">gi 86131801 ref ZP_01050398.1 </a>	putative ATP-dependent DNA helica	<a href="#">35.8</a>	5.5	
<a href="#">gi 41053341 ref NP_956318.1 </a>	DEAH (Asp-Glu-Ala-His) box polypept	<a href="#">35.8</a>	5.6	<b>U/G</b>
<a href="#">gi 77361139 ref YP_340714.1 </a>	ATP-dependent helicase [Pseudoalter	<a href="#">35.8</a>	5.6	<b>G</b>
<a href="#">gi 82495358 ref ZP_00880934.1 </a>	ATP-dependent helicase HrpB [Shew	<a href="#">35.4</a>	5.7	
<a href="#">gi 103485877 ref YP_615438.1 </a>	peptidase S1 and S6, chymotryps...	<a href="#">35.4</a>	5.8	<b>G</b>
<a href="#">gi 50546625 ref XP_500782.1 </a>	hypothetical protein [Yarrowia lipo	<a href="#">35.4</a>	6.2	<b>G</b>
<a href="#">gi 27375353 ref NP_766882.1 </a>	ATP-dependent DNA helicase [Bradyrh	<a href="#">35.4</a>	6.4	<b>G</b>

gi 76646513 ref XP_869834.1	PREDICTED: similar to Probable A...	35.4	6.4	G
gi 86360653 ref YP_472541.1	hypothetical protein RHE_PE00379 [R	35.4	6.5	G
gi 68483511 ref XP_714316.1	putative rRNA biogenesis helicase...	35.4	7.0	G
gi 68484077 ref XP_714041.1	putative rRNA biogenesis helicase...	35.4	7.0	G
gi 37520933 ref NP_924310.1	probable helicase protein [Gloeobac	35.4	7.0	G
gi 46137751 ref XP_390567.1	conserved hypothetical protein [Gib	35.4	7.0	G
gi 92118900 ref YP_578629.1	ATP-dependent DNA helicase RecQ [Ni	35.4	7.1	G
gi 33151690 ref NP_873043.1	ATP-dependent DNA helicase [Haemoph	35.4	7.3	G
gi 13473449 ref NP_105016.1	DNA helicase RecQ [Mesorhizobium lo	35.4	7.3	G
gi 85060315 ref YP_456017.1	ATP-dependent DNA helicase RecQ ...	35.0	7.6	G
gi 91794513 ref YP_564164.1	ATP-dependent helicase HrpB [Shewan	35.0	7.6	G
gi 37528437 ref NP_931782.1	ATP-dependent DNA helicase RecQ ...	35.0	7.8	G
gi 83313353 ref YP_423617.1	Superfamily II DNA helicase [Magnet	35.0	8.0	G
gi 88948137 ref ZP_01150900.1	Helicase, C-terminal:DEAD/DEAH...	35.0	8.0	
gi 6323844 ref NP_013915.1	Nucleolar DNA helicase of the Rec...	35.0	8.7	G
gi 39972399 ref XP_367590.1	hypothetical protein MG07501.4 [Mag	35.0	9.0	G
gi 85373654 ref YP_457716.1	serine protease, putative [Erythrob	35.0	9.0	G
gi 71420156 ref XP_811384.1	aminoacylase [Trypanosoma cruzi str	35.0	9.2	G
gi 62326966 ref YP_224077.1	gpl [Cucumber vein yellowing virus]	35.0	9.3	
gi 74009225 ref YP_308881.1	CI protein [Cucumber vein yellowing	35.0	9.3	
gi 19921526 ref NP_609946.1	CG10689-PA [Drosophila melanogaster	35.0	9.4	UG
gi 15603292 ref NP_246366.1	RecQ [Pasteurella multocida subsp.	35.0	9.6	G
gi 68249329 ref YP_248441.1	ATP-dependent DNA helicase RecQ ...	35.0	9.6	G
gi 46133102 ref ZP_00156591.2	COG0514: Superfamily II DNA he...	35.0	9.6	
gi 16272669 ref NP_438887.1	ATP-dependent DNA helicase [Haemoph	35.0	9.6	G
gi 94311396 ref YP_584606.1	amidophosphoribosyltransferase [Ral	34.7	9.9	G

## Alignments

Get selected sequences	Select all	Deselect all	Distance tree of results
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>  gi|22129793|ref|NP\_671491.1| polyprotein [Hepatitis C virus]  
Length=3011

Score = 1286 bits (3328), Expect = 0.0, Method: Composition-based stats.  
Identities = 670/685 (97%), Positives = 678/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266